



20010-04USA.ST25.txt

SEQUENCE LISTING

<110> POSCO
POSTECH
An, Gynheung
Ryu, Choong-Hwan
Han, Jong-Jin
Kang, Hong-Gyu
An, Kyungsook

<120> ORGAN PREFERENTIAL GENES IDENTIFIED BY T-DNA INSERTIONAL
MUTAGENESIS OF RICE

<130> 20010-04USA

<140> US 10/713,648

<141> 2003-11-14

<150> 60/427,166

<151> 2002-11-15

<160> 83

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 474

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (394)...(474)

<223> segment of the T-DNA insert in line 1B-115-22

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caagcataaa	tagcagcgtc	ccctgcttcc	tttcttcatac	gtcctcagct	catcatctgc	240
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gccaaagctga	tcctcgccac	cttcgccgctc	gtgttaccag	gtaccagggtg	agttccattc	420
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<210> 2

<211> 194

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (104)...(194)

<223> segment of the T-DNA insert in line 1B-164-43

<400> 2

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gtaatttttg	tttgattttc	tccgcagcca	tgggagacct	acacggatcc	gaggtaccag	120
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 <213> Oryza sativa

<220>
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 <223> segment of the T-DNA insert in line 1B-192-40

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 caaactcaca ggcaggatcc catctacact tggttcttgc gtccggttgg aatcgcttcg 120
 tgtaggaggc aacttcctag agggaagtat tccacaatca ttagcaaatc tcaggggcac 180
 caaagtgctg gatttctccc agaacaattt atctggtgca ataccggatt tctttgggac 240
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 tgtggctaatac tacatgacta acttg 325

<210> 4
 <211> 650
 <212> DNA
 <213> Oryza sativa

<220>
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 <222> (560)...(650)
 <223> segment of the T-DNA insert in line 1B-207-27

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 tcccattgag agtgcaaaat ctactcaac ttactgcatt gcttctccag aataactctc 180
 tttctggacc catccctgac ctccaactcc caaaattgag gcatttgaat ttgagcaaca 240
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 cgtcaaaagg aaaaactgtt ggatccgagg taccaggtac caggtgagtt ccattcttac 600
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<210> 5
 <211> 6721
 <212> DNA
 <213> Oryza sativa

<220>
 <221> misc_feature
 <222> (1311)...(1400)
 <223> segment of the T-DNA insert in line 1B-138-07

<400> 5
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 ggcctccgcc ggcctcccat ggccgcgccg ctctccaccg ccgcccgcgc ctctgtgctc 180
 tccgacagcg cctcgtctcc ggtaagcacc cgcgcgccgc tcatccattc ccaatttccc 240
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 gggattggag agctagaagc ttcactcgat gatgtggttg gatcatgtta tagtgattct 720

20010-04USA.ST25.txt

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20010-04USA.ST25.txt

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 <211> 232
 <212> DNA
 <213> Oryza sativa
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 <222> (1)...(101)
 <223> segment of the T-DNA insert in line 1D-059-12

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aaaacgtccg	caatgtgtta	tttaagttgtc	taagcgtcaa	ggagagcgag	gatggccgta	120
aggattcgtc	tcctctcctt	tttgttcattg	atcctgtctg	tgtgtgattc	tggaattctg	180
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<210> 7
 <211> 246
 <212> DNA
 <213> Oryza sativa
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 <223> segment of the T-DNA insert in line 1C-087-40

20010-04USA.ST25.txt

<400> 7
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 accaattaat gtttgatgtt catttcattc aaacacggat ccgaggtacc aggtaccagg 180
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<210> 8
 <211> 370
 <212> DNA
 <213> Oryza sativa

<220>
 <221> misc_feature
 <222> (1)...(218)
 <223> segment of the T-DNA insert in line 1C-017-14

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 aaaacgtccg caatgtgta ttaagttgtc taagcgtcaa gttgtctcga gaattcagcg 120
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 atatttttca caaaaaatag tcggtatgta tttacattgt aactccttaa attacatag 300
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<210> 9
 <211> 214
 <212> DNA
 <213> Oryza sativa

<220>
 <221> misc_feature
 <222> (126)...(214)
 <223> segment of the T-DNA insert in line 1C-038-56

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 gttctgaaga tggacctgac ctgttggttg gtctcttcag agtttttagg agttgagaca 120
 aagcctatcc gaggtaccag gtaccagggt agttccattc ttactaccac ggtgctatatt 180
 tttttgctat gtggctaatt acatgactaa cttg 214

<210> 10
 <211> 514
 <212> DNA
 <213> Oryza sativa

<220>
 <221> misc_feature
 <222> (1)...(113)
 <223> segment of the T-DNA insert in line 1C-041-47

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 tattgatatc aataaattta gatagatata tatgtctgaa tttttgcttt tcctcttctc 120
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<210> 11
 <211> 603
 <212> DNA
 <213> Oryza sativa

<220>
 <221> misc_feature
 <222> (512)...(603)
 <223> segment of the T-DNA insert in line 1C-064-20

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<210> 12
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 <212> DNA
 <213> Oryza sativa

<220>
 <221> misc_feature
 <222> (1)...(96)
 <223> segment of the T-DNA insert in line 1C-109-35

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 atttttcttt tccgtacaac acacgaatct caataaaata t 401

<210> 13
 <211> 628
 <212> DNA
 <213> Oryza sativa

<220>
 <221> misc_feature
 <222> (528)...(628)
 <223> segment of the T-DNA insert in line 1C-109-51

<400> 13
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 taagtgtatct ggaacaggaa gttgtaactc agctgtttct cagtgggagg atccaagtgt 180
 gtgttgcgag tagcactgtg tgctggggaa gatcattgcc tgcccatctg gtggttggtga 240
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 tactccaaat gatgggtcat gctagcaggc ctcttcaaga taactcaggg aaatgtgtta 360
 tattgtgtca tgcgcctcgc aaggaatact acaagaagtt cttttttgag gccttccttg 420
 ttgagagcca tcttcaccac ttcttgcatg atcatatgaa cgctgagggtg gtggttggtg 480
 tcatagaaaa caagcaagat gctgtggatt accttacttg gaccttcatg tcaaacacgg 540
 atccgaggta ccaggtacca ggtgagttcc attcttacta ccacggtgct attttttttg 600

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628

<210> 14

<211> 377

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (1)...(61)

<223> segment of the T-DNA insert in line 1C-056-07

<400> 14

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cattttctac gtgatccatt caaccactgc agtgaccttc aatgttgctg gcaacctgaa 300
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gaactgatca ttgcgct                                     377

```

<210> 15

<211> 422

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (351)...(422)

<223> segment of the T-DNA insert in line 1C-100-32

<400> 15

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ctaaactgac cactcttata agttttatta ctttatactg tagatgtctt gctgtcctgt 60
aactcaatat gctaccact aatatctagg agttaccatt gtactaaaaa tgtataaaac 120
atggttgata ggagttcaga aagtgcattt atctgggtac atccgatcac tggtagaata 180
tgttaccact tgaaccaaac tttatgtaat ttataatggg atatttgcaa ctacggaatc 240
ttttactgct catgcaggat cacaaaggaa tttcaaatgc tgcaccagct gattgtccat 300
tgatcccact attggtgcc aagtagatc aatcagaagg tacagtggat accaggtgag 360
ttccattctt actaccacgg tgctattttt tttgctatgt ggctaattac atgactaact 420
tg                                     422

```

<210> 16

<211> 335

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (259)...(335)

<223> segment of the T-DNA insert in line 1C-142-27

<400> 16

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ttggttcgat agcaaccgct gcagttgcaa atttgcaata ttgttttagcg agtagcagcc 120
tgcactgtcg ttgattgagg attcgttgct tgttttgcct accgtcatgg gcctttttca 180
ggtcaccgac cgcacagagg ataagagcca agattctgta cgcgacgtcg aagcaagggc 240
tgaggcgggt gcttgacgga ggtaccaggt gagttccatt cttactacca cggtgctatt 300
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```

<210> 17

<211> 425

<212> DNA

<213> Oryza sativa

<220>
 <221> misc_feature
 <222> (332)...(425)
 <223> segment of the T-DNA insert in line 1C-140-04

<400> 17
 gctttccagg tatatatata taaaatccat cgatcatgca tgtcagaagc tcatcatgct 60
 cagatgctca tcctgctcac gctcaatgct catgctctgc tgaaatttgg cggaatttgt 120
 tgcacggat ttgtgtttcc gtattgcatc atgtttgtat atgccaagat atgtgcttac 180
 taccgtgtga gcaatgctgt tcaagaactg aattttgttt tgcaaatgtg tcacacctgg 240
 agtaggtgga aggggcagct gcagaggatg ggaggaagcc cagcatttgg gacaccttca 300
 tccatcaagg tccaaaaaaa tggagtagat gacacggatc cgaggtacca ggtaccaggt 360
 gagttccatt cttactacca cggtgctatt ttttttgcta tgtggctaata tacatgacta 420
 acttg 425

<210> 18
 <211> 1149
 <212> DNA
 <213> Oryza sativa

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> line 1B-115-22 - genomic DNA without T-DNA insert

<221> misc_feature
 <222> (394)...(395)
 <223> location in genomic DNA where T-DNA was inserted
 to create line 1B-115-22

<400> 18
 aagcttaata tattaggagt agtaagctag cgtgtgagga agattcataa ccatatatca 60
 tcttaattag cctttgtgat tttagcttaat cacatggcta aggcacaacc acccatccac 120
 ttaactcttc attactacgc tagctacacg aggagagtag ctagctagta caggccccgg 180
 caagcataaa tagcagcgtc ccctgcttcc tttcttcacg gtcctcagct catcatctgc 240
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 cagctacttc actttgcata gtttgatcga actaaataac tcaccaagtt agctgtaatg 360
 gccaaagtga tcctcgccac cttcgccgct gtgttcattg cgctcgccgc cacctccctc 420
 gccggcgacc cggacatgct ccaggacgtc tgcgtcgccg actacaagtc cctcaaaggc 480
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 aaatactag 1149

<210> 19
 <211> 2971
 <212> DNA
 <213> Oryza sativa

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> line 1B-164-43 - genomic DNA without T-DNA insert

<221> misc_feature
 <222> (577)...(578)
 <223> location in genomic DNA where T-DNA was inserted
 to create line 1B-164-43

<400> 19

```

caaaaaggcg cctctaagaa ttcttcccaa actttttggt gttgtcaagc cgtgcgtttc 60
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tcggcggcgt ccgcctcttc accgcgtcgg cgacctctcc ggcggcggcg ggcggcggcg 180
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<210> 20
 <211> 4566
 <212> DNA
 <213> Oryza sativa

<220>

<221> misc_feature
 <222> (0)...(0)
 <223> line 1B-192-40 - genomic DNA without T-DNA insert

<221> misc_feature
 <222> (2273)...(2274)
 <223> location in genomic DNA where T-DNA was inserted
 to create line 1B-192-40

```

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<210> 21

<211> 1914

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1B-207-27 - genomic DNA without T-DNA insert

<221> misc_feature

<222> (906)...(907)

<223> location in genomic DNA where T-DNA was inserted
to create line 1B-207-27

<400> 21

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<211> 6631

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<222> (0)...(0)

<223> line 1B-138-07 - genomic DNA without T-DNA insert

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<223> location in genomic DNA where T-DNA was inserted
to create line 1B-138-07

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<213> Oryza sativa

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<223> line 1D-059-12 - genomic DNA without T-DNA insert

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<223> location in genomic DNA where T-DNA was inserted
to create line 1D-059-12

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<223> location in genomic DNA where T-DNA was inserted
to create line 1C-087-40

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<223> location in genomic DNA where T-DNA was inserted
to create line 1C-017-14

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<210> 26

<211> 2034

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1C-038-56 - genomic DNA without T-DNA insert

<221> misc_feature

<222> (125)...(126)

<223> location in genomic DNA where T-DNA was inserted
to create line 1C-038-56

<400> 26

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<210> 27

<211> 4284

<212> DNA

<213> Oryza sativa

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> line 1C-041-47 - genomic DNA without T-DNA insert

<221> misc_feature
 <222> (2471)...(2472)
 <223> location in genomic DNA where T-DNA was inserted
 to create line 1C-041-47

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<210> 28

<211> 3234

<212> DNA

<213> *Oryza sativa*

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1C-064-20 - genomic DNA without T-DNA insert

<221> misc_feature

<222> (2690)...(2691)

<223> location in genomic DNA where T-DNA was inserted
to create line 1C-064-20

<400> 28

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<210> 29

<211> 3677

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1C-109-35 - genomic DNA without T-DNA insert

<221> misc_feature

<222> (2301)...(2302)

<223> location in genomic DNA where T-DNA was inserted
to create line 1C-109-35

<400> 29

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<222> (6570)...(6571)

<223> location in genomic DNA where T-DNA was inserted
to create line 1C-109-51

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<213> Oryza sativa

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<223> line 1C-056-07 - genomic DNA without T-DNA insert

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to create line 1C-056-07

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<211> 7726

<212> DNA

<213> Oryza sativa

<220>

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<221> misc_feature

<222> (5051)...(5052)

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to create line 1C-100-32

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to create line 1C-142-27

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 tttatgtacc aagaccaaag ataatttaaa tcacatcaat caagatatca tgcacatatt 2760
 ctcccacaat gcatgcatcg attaaaatc cataccaatt acaccttaat atgcagacat 2820
 tcttccatgt tgtattaatt atgttatgat gaaatctatg tccatgtggg tatatgatat 2880
 tcaatttaag aaattttgaa ttccattata tgatgatcaa tttggaaagg agggagtatt 2940

20010-04USA.ST25.txt

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tctgtatctt ctgaccgtgt atatccactt gtgcgagcct gtgaggtcag atttctatca 3000
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accggttaca aatcgggtcat t 4941

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<210> 35

<211> 672

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1B-115-22 coding sequence

<400> 35

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ggcccgtgct ggctgaacgg gttcccgtgc aagaggatag agaactgac ggcgaacgac 180
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atcgactacg cgccatgggg gctgaaccca ccgcacacgc atccccgtgc caccgagatc 360
atcttcgtcg tcgagggtc cctcgacgtc ggcttcgtca ccaccgcaa caagctcttc 420
acctgcaccg tctgcaaggg ggaggtgttc gtcttcccgc gggggctcgt ccacttccag 480
aagaacaacg gcaacacgcc ggcgttcgcc atcgccgcct tgaacagcca gctccccggg 540
acgcagtcca tcgccgccgc gctcttcggc gccgcgccgc cgctgccgtc ggacacgctg 600
gccaggcggt tccaggtcga cggcggcatg gtcgagttca tcaagtccaa gttcgtcccc 660
cccaaatact ag 672

```

<210> 36

<211> 999

<212> DNA

<213> Oryza sativa

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> line 1B-164-43 coding sequence

<400> 36
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 ggcggagaag ccgtcccccgg ggtgtggggg ttgcggctga tgtccacgtc gtccgtggcg 180
 tcgacggagg cggcggccaa ggcgagggcc aagaaggcgg acgcgagaa ggaggtggtg 240
 gtcaacagct actggggcat cgagcagtcg aagaagctgg tgcgggagga cggcacggag 300
 tggaagtggg cttgcttttag gccatgggag acctacaccg cggacacttc gatcgatctg 360
 acgaagcacc acgtgcccaa gacgctgctc gacaagatcg cctactggac cgtcaagtcg 420
 ctgcgcttcc ccactgatata cttcttccag aggaggtatg gctgccgcgc gatgatgctg 480
 gagacggtgg cggcggtgcc ggggatgggt ggcggcatgc tgcctcacct ccggtccctc 540
 cggcgcttcg agcagagcgg cggctggatc cgacgctgc tggaaaggcc cgagaacgag 600
 cgcattgcacc tgatgacctt catggaggtg gcgaacccaa agtggtagca gcgcgccctc 660
 gtcattaccg tccagggcgt cttcttcaac gcctacttcc tgggttacct cctctcccc 720
 aagttcgcg accgcgtcgt cggctacctc gaggaggagg ccatccactc gtacaccgag 780
 ttctctaagg acctcgaggc cggcaagatc gacaacgtcc ctgccccggc catcgccatc 840
 gactactggc gcctccccgc caacggacg ctcaaggacg tcgtcaccgt cgtgcgcgcc 900
 gacgaggctc accaccgcga cgtcaatcac ttgcattcgg acatccatta ccagggcag 960
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<210> 37
 <211> 3216
 <212> DNA
 <213> Oryza sativa

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> line 1B-192-40 coding sequence

<400> 37
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 gcaatagctg acgaatccga caataaccaa cgggaagctc tgctctgcat caaatcacac 120
 ctctcaagcc cagaggagg cgccctcacc acatggaaca atacctcgct cgacatgtgc 180
 acctggcgcg cgtgacatg ctccagcagc ctcccaaagc ctcgtttggt cgtggccttg 240
 gacatggagg cacagggcct cagcggagaa atcccaccct gcatctccaa cctctcgtcc 300
 ctcacgagaa tccacctccc caacaatggc ctctccggtg gcctcgcac cgcagccgat 360
 gttgccgggc tccgatacct caacctcagc ttcaacgcga tcggcggtgc gatcccaaaa 420
 cgccttggtg cgcttcgcaa ctttctgtcc ctggacttaa caaacaacaa cattcatggc 480
 gagatcccg cggtgcttg gagctcatct gccttggaa cctcgtgtct cgcgacaac 540
 tacctgaccg gaggaatccc attgttcttg gctaattgcg cctcgtccg ctatctttcc 600
 ttgaagaaca atagcctcta tgggagcatc cctgcagcac ttttcaacag ctcaaccatc 660
 agggaaatat accttgaga aaacaatctt tctggtgcaa ttccaccctg aacaatattc 720
 ctttcccaga tcaccaacct tgattcttaca acgaatagcc tgacaggagg cataccacca 780
 tctctagga atctctcat gcttacagca ctcttagctg cagaaaacca gttgcaggga 840
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 tctagcatat ccctacttta tcttggtaac aatctattga caggagcat acctcatact 1440
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 ataccacaat ccattggtaa cttgaatcga ttgactgaac tctatttagc agaaaatcaa 1560
 ctgactggaa gaatacctgc aactttatcg aggtgccaac aattgttggc attgaacctt 1620

20010-04USA.ST25.txt

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actgtctgct	ctgcttcagc	atccaaaaga	aagaataagc	tcattattcc	aatgttgga	2160
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cgatgcaaac	tgggaggggt	ggaggggtatt	ctcacatgta	cgataagaga	aattgcatca	3180
aaattaggag	ggcttagatt	atctatgcta	acgtga			3216

<210> 38

<211> 1914

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1B-207-27 coding sequence

<400> 38

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ctgccacatg	gcaggaagct	caactggagc	tctgcagccc	cagtctgcac	ttcatgggtt	180
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cttaggtcca	atcgcatcac	tgttgatctc	cctctgaag	taggatccat	tccttctctc	360
cattccctat	atcttcagca	taataaccta	tccgggatca	taccgacttc	ccttacttcc	420
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gagggaggcg	ggaagttcat	ccatggcaac	ctcaagtcac	caaacatcct	tctgtcacag	1440

20010-04USA.ST25.txt

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aacctcgacg gctgtgtctc tgagtttggg ctggcacagc ttatgaccat tccaccagct 1500
ccagcacgcc ttgtcggata tcgtgcacca gaagtcctcg agactaaaaa gccaaccag 1560
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caacggccaa aaatggacga ggtgatcagg aggatcggtg agatccgaa ttcctactcc 1860
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<210> 39

<211> 1571

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1B-138-07 coding sequence

<400> 39

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gacgagttca gggccgccgt ggacgccgcc aggaccgcct tccccgggtg gcggaacacg 240
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gataaactgg cagagaacat tacaaccgaa caggggaaga cactgaagga tgcttggggc 360
gatgtattcc gtgggctagg tgggtgaaca tgcttgtgga atggggacac tgcagatggg 420
tgaatatgta tcaaagtgtt ctaacgggat tgacaccttt agcattaggg agccacttgg 480
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ttgcaggaga cttgaatttc tacggcaagg cgggcgtgca gttcttcacc cagatcaaga 1500
cggtcacgca gcagtggaag gagtgcggcg ctgagcgctg ctccctctcc atgccacct 1560
cgcagaagtg a

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<210> 40

<211> 1323

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1D-059-12 coding sequence

<400> 40

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cgccagggtg agttctactt cagcgacagc aacctcccc gcgacaactt cctgcggaag 120
acagtcgagg agagcgagga tggcgtgagc ttggcactca tctgctcctt ctgcgggatg 180
aagaagcacc taggcctgga cgcgagcgtg aagcaggaga ccatgccgga ggagacggtg 240

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20010-04USA.ST25.txt

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ctcgccgttg ctgaggtgct gcggcggttcc tcggccctcc gtgtcaccga ggataagaaa 300
gttggttagat caattgagtt gtcgaaactg gatgagatca tggagcaagt ggactctagg 360
acaattgctg catcaccatt tccttacaat gtaaagctgg aagatgttca gtctttcttt 420
gctcagtatg gcaaggtgaa cagtgtgagg ctacctcgac atattgccga caaacgacac 480
ttctgtggca ctgctttagt cgaattttca gaagaagagg aagcaaatgc tgtattaaag 540
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gcagaaaatg gtggggacaa agaggggtgaa actgatgatg ccaataaatc aagaacaggg 780
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cataatgcac ctagaatgaa tcttaggagt gggctgaaac ttaaaataga agttgaagcc 1260
ttatggcaca caagaatgcc aacacatata tttggagtta tattatcatg gaactggcag 1320
taa 1323

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<210> 41

<211> 2568

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1C-087-40 coding sequence

<400> 41

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tctctctggg cgcgcctcca ggactccatc tcgcgccact ccttcgacac gccgctctac 120
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20010-04USA.ST25.txt

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<210> 42

<211> 1413

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1C-017-14 coding sequence

<400> 42

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<210> 43

<211> 1227

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1C-038-56 coding sequence

<400> 43

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ccgcagccgg gcggcgaggc ggcgagccat cagcagcagc agaaggagat gaagctgaag 180
aagccggaca agatcctgcc atgcccgcgg tgcagcagca tggacaccaa gttctgctac 240

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20010-04USA.ST25.txt

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tccgcgacct	tccaggaggg	atcttga				1227

<210> 44

<211> 861

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1C-041-47 coding sequence

<400> 44

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<210> 45

<211> 1653

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1C-064-20 coding sequence

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aagctttggc	cttcaaaagt	cgtggcaggt	caagaggaca	ggccgatgat	cgtgggtgag	360
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20010-04USA.ST25.txt

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<210> 46
 <211> 1437
 <212> DNA
 <213> Oryza sativa

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> line 1c-109-35 coding sequence

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<210> 47
 <211> 6534
 <212> DNA
 <213> Oryza sativa

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> line 1C-109-51 coding sequence

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20010-04USA.ST25.txt

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<211> 543

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1C-056-07 coding sequence

<400> 48

atggttggtc gccttgctac atctaccaag accattttgg cagagtctct actccacgga 60

20010-04USA.ST25.txt

tacaaatttg	acattaacac	agtgtactac	atggcaccct	ttgccaccat	gatactggct	120
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ttgatctctc	aacagcaggc	tgtagctcca	ggaacaggaa	gccaacaac	atcgcaaaca	480
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taa						543

<210> 49

<211> 2436

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1c-100-32 coding sequence

<400> 49

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gccaacaaca	ccggcggtgc	ccagcaccac	atgtggaaga	ccagcctctg	ctccttcttc	180
cgccgcccgc	ccgcctcctc	cgccgacggc	tgcagccacg	gcgactcctg	ccgctacgcg	240
cactccgagg	aggagctccg	cccgcgcccc	gacggcacct	gggacccac	ctccgaccgc	300
gccaagaagc	tccgcaaggt	cgccgcccgc	gaggtggagg	aagaggtggt	caccattgac	360
gacaaggccc	tggacaagtg	cctcgtcggc	ctcccagggg	gatgggccaa	cgacaggctc	420
aagactttcc	tccaagacaa	ggcaagaact	aactactcct	ccattcttcc	tcctgctcta	480
ctactaggaa	tctcgtatgc	aacagcgaag	aagaagaagg	gaatgactgt	tggttttgta	540
acttttgaaa	atattgaaca	gctgaagaat	gctatcgagg	tacttacaga	gaaccaatct	600
ggtggaaagg	aaataaagat	agcagatgcc	aatcgtagat	ctcatcaaaa	gctgcacaca	660
gaaaagcctg	tatctgacaa	tggagtgaac	acagaaaatg	gtactagtgt	tgatgttctc	720
cctggggaga	catctgcacc	tgaagcagca	atatcaaata	aaaaaagtgt	ccgcatgcca	780
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gcgcagatac	tgaagaggct	tactcgcaat	gctaggaaag	cttgccctac	tggcattccc	900
cttccagatt	gggtttttta	atccaaagaa	atttttcatt	tattccattt	ttcctcttta	960
gtttgtcatg	atttatattt	aaatcatgca	ggtggtcttc	cttgcaagct	tgaaggcatt	1020
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gcatcattga	tcaatgagtc	tgttgacctg	aaagtatcgg	actgtttgga	ggacagaaag	2280
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<210> 50
 <211> 429
 <212> DNA
 <213> Oryza sativa

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> line 1C-142-27 coding sequence

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atggcaatgg cttacaagat ggcgacggag gggatgaacg tgaaggagga gtgccagagg 60
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cggtcgcgcg ccgtgctggg ggacaagggt ggcgccccg gcgaagggtg cgaggagctc 180
gtcgccgcgc tgcccaccga cgactgccgc tacgccgtct tcgacttcga cttcgtcacc 240
gtcgacaact gccagaagag caagatcttc ttcatcgctt caccgaccgc atcgaggata 300
agagccaaga ttctgtacgc gacgtcgaag caagggtgta ggcggggtgct tgacgggggtc 360
cactacgagg tgcaagccac ggactcctcc gagatgggct acgacgtcat ccgaggccgc 420
gctcagtga                                     429
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<210> 51
 <211> 1344
 <212> DNA
 <213> Oryza sativa

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> line 1C-140-04 coding sequence

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<400> 51
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cttgggtcgt tggcgagaga ggcttctgcy ctcacccggc atgacttccc cgagggtctc 120
gtcttcggcg caggctcctc cgctttccag gtggaagggg cagctgcaga ggatgggagg 180
aagcccagca tttgggacac cttcatccat caatacatgc ctgacggctc caatgcagat 240
gtctcagcag atcagtatca ccattacaag gaggatgtaa agcttatgta tgacatgggg 300
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ctttgtgctg gtaaaggaag ttga                                     1344
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<210> 52
 <211> 223
 <212> PRT
 <213> Oryza sativa

<220>
 <221> PEPTIDE
 <222> (0)...(0)

<223> line 1B-115-22 polypeptide sequence

<400> 52

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Met Ala Lys Leu Ile Leu Ala Thr Phe Ala Val Val Phe Met Ala Leu
 1      5      10      15
Ala Ala Thr Ser Leu Ala Gly Asp Pro Asp Met Leu Gln Asp Val Cys
 20      25      30
Val Ala Asp Tyr Lys Ser Leu Lys Gly Pro Leu Arg Leu Asn Gly Phe
 35      40      45
Pro Cys Lys Arg Ile Glu Asn Val Thr Ala Asn Asp Phe Phe Phe Asp
 50      55      60
Gly Leu Met Lys Ala Gly Asn Thr Gly Asn Ala Val Gly Ser Val Val
 65      70      75      80
Thr Ala Ala Ser Val Glu Ser Leu Pro Gly Leu Asn Thr Met Gly Val
 85      90      95
Ser Met Ala Arg Ile Asp Tyr Ala Pro Trp Gly Leu Asn Pro His
100      105      110
Thr His Pro Arg Ala Thr Glu Ile Ile Phe Val Val Glu Gly Ser Leu
115      120      125
Asp Val Gly Phe Val Thr Thr Ala Asn Lys Leu Phe Thr Arg Thr Val
130      135      140
Cys Lys Gly Glu Val Phe Val Phe Pro Arg Gly Leu Val His Phe Gln
145      150      155      160
Lys Asn Asn Gly Asn Thr Pro Ala Phe Ala Ile Ala Ala Leu Asn Ser
165      170      175
Gln Leu Pro Gly Thr Gln Ser Ile Ala Ala Ala Leu Phe Gly Ala Ala
180      185      190
Pro Pro Leu Pro Ser Asp Thr Leu Ala Arg Ala Phe Gln Val Asp Gly
195      200      205
Gly Met Val Glu Phe Ile Lys Ser Lys Phe Val Pro Pro Lys Tyr
210      215      220

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<210> 53

<211> 332

<212> PRT

<213> Oryza sativa

<220>

<221> PEPTIDE

<222> (0)...(0)

<223> line 1B-164-43 polypeptide sequence

<400> 53

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Met Ser Ser Arg Met Ala Gly Ser Ala Ile Leu Arg His Val Gly Gly
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Val Arg Leu Phe Thr Ala Ser Ala Thr Ser Pro Ala Ala Ala Ala Ala
 20      25      30
Ala Ala Ala Arg Pro Phe Leu Ala Gly Gly Glu Ala Val Pro Gly Val
 35      40      45
Trp Gly Leu Arg Leu Met Ser Thr Ser Ser Val Ala Ser Thr Glu Ala
 50      55      60
Ala Ala Lys Ala Glu Ala Lys Lys Ala Asp Ala Glu Lys Glu Val Val
 65      70      75      80
Val Asn Ser Tyr Trp Gly Ile Glu Gln Ser Lys Lys Leu Val Arg Glu
 85      90      95
Asp Gly Thr Glu Trp Lys Trp Ser Cys Phe Arg Pro Trp Glu Thr Tyr
100      105      110
Thr Ala Asp Thr Ser Ile Asp Leu Thr Lys His His Val Pro Lys Thr
115      120      125
Leu Leu Asp Lys Ile Ala Tyr Trp Thr Val Lys Ser Leu Arg Phe Pro
130      135      140
Thr Asp Ile Phe Phe Gln Arg Arg Tyr Gly Cys Arg Ala Met Met Leu

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20010-04USA.ST25.txt

145	Glu	Thr	Val	Ala	Ala	Val	Pro	Gly	Met	Val	Gly	Gly	Met	Leu	Leu	His
				165						170					175	
	Leu	Arg	Ser	Leu	Arg	Arg	Phe	Glu	Gln	Ser	Gly	Gly	Trp	Ile	Arg	Thr
				180					185					190		
	Leu	Leu	Glu	Glu	Ala	Glu	Asn	Glu	Arg	Met	His	Leu	Met	Thr	Phe	Met
				195				200					205			
	Glu	Val	Ala	Asn	Pro	Lys	Trp	Tyr	Glu	Arg	Ala	Leu	Val	Ile	Thr	Val
				210			215					220				
	Gln	Gly	Val	Phe	Phe	Asn	Ala	Tyr	Phe	Leu	Gly	Tyr	Leu	Leu	Ser	Pro
	225					230					235					240
	Lys	Phe	Ala	His	Arg	Val	Val	Gly	Tyr	Leu	Glu	Glu	Glu	Ala	Ile	His
				245						250					255	
	Ser	Tyr	Thr	Glu	Phe	Leu	Lys	Asp	Leu	Glu	Ala	Gly	Lys	Ile	Asp	Asn
				260					265					270		
	Val	Pro	Ala	Pro	Ala	Ile	Ala	Ile	Asp	Tyr	Trp	Arg	Leu	Pro	Ala	Asn
				275				280					285			
	Ala	Thr	Leu	Lys	Asp	Val	Val	Thr	Val	Val	Arg	Ala	Asp	Glu	Ala	His
				290			295					300				
	His	Arg	Asp	Val	Asn	His	Phe	Ala	Ser	Asp	Ile	His	Tyr	Gln	Gly	Met
	305				310						315					320
	Glu	Leu	Lys	Gln	Thr	Pro	Ala	Pro	Ile	Gly	Tyr	His				
				325						330						

<210> 54

<211> 1073

<212> PRT

<213> Oryza sativa

<220>

<221> PEPTIDE

<222> (0)...(0)

<223> line 1B-192-40 polypeptide sequence

<400> 54

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			20					25					30		
Ala	Leu	Leu	Cys	Ile	Lys	Ser	His	Leu	Ser	Ser	Pro	Glu	Gly	Gly	Ala
			35				40					45			
Leu	Thr	Thr	Trp	Asn	Asn	Thr	Ser	Leu	Asp	Met	Cys	Thr	Trp	Arg	Gly
			50			55					60				
Val	Thr	Cys	Ser	Ser	Glu	Leu	Pro	Lys	Pro	Arg	Leu	Val	Val	Ala	Leu
65					70				75						80
Asp	Met	Glu	Ala	Gln	Gly	Leu	Ser	Gly	Glu	Ile	Pro	Pro	Cys	Ile	Ser
				85					90					95	
Asn	Leu	Ser	Ser	Leu	Thr	Arg	Ile	His	Leu	Pro	Asn	Asn	Gly	Leu	Ser
			100					105					110		
Gly	Gly	Leu	Ala	Ser	Ala	Ala	Asp	Val	Ala	Gly	Leu	Arg	Tyr	Leu	Asn
			115				120					125			
Leu	Ser	Phe	Asn	Ala	Ile	Gly	Gly	Ala	Ile	Pro	Lys	Arg	Leu	Gly	Thr
			130			135					140				
Leu	Arg	Asn	Leu	Ser	Ser	Leu	Asp	Leu	Thr	Asn	Asn	Asn	Ile	His	Gly
145					150					155					160
Glu	Ile	Pro	Pro	Leu	Gly	Ser	Ser	Ser	Ala	Leu	Glu	Ser	Val	Gly	
				165				170					175		
Leu	Ala	Asp	Asn	Tyr	Leu	Thr	Gly	Gly	Ile	Pro	Leu	Phe	Leu	Ala	Asn
			180					185					190		
Ala	Ser	Ser	Leu	Arg	Tyr	Leu	Ser	Leu	Lys	Asn	Asn	Ser	Leu	Tyr	Gly
		195					200					205			
Ser	Ile	Pro	Ala	Ala	Leu	Phe	Asn	Ser	Ser	Thr	Ile	Arg	Glu	Ile	Tyr

20010-04USA.ST25.txt

210	215	220
Leu Gly Glu Asn Asn	Leu Ser Gly Ala Ile Pro	Pro Val Thr Ile Phe
225	230	235
Pro Ser Gln Ile Thr	Asn Leu Asp Leu Thr	Asn Ser Leu Thr Gly
245	250	255
Gly Ile Pro Pro Ser	Leu Gly Asn Leu Ser Ser	Leu Thr Ala Leu Leu
260	265	270
Ala Ala Glu Asn Gln	Leu Gln Gly Ser Ile Pro	Asp Phe Ser Lys Leu
275	280	285
Ser Ala Leu Arg Tyr	Leu Asp Leu Ser Tyr Asn	Asn Leu Ser Gly Thr
290	295	300
Val Asn Pro Ser Val	Tyr Asn Met Ser Ser Ile	Thr Phe Leu Gly Leu
305	310	315
Ala Asn Asn Asn Leu	Glu Gly Ile Met Pro Pro	Gly Ile Gly Asn Thr
325	330	335
Leu Pro Asn Ile Gln	Val Leu Ile Met Ser Asp	Asn His Phe His Gly
340	345	350
Glu Ile Pro Lys Ser	Leu Ala Asn Ala Ser Asn	Met Gln Phe Leu Tyr
355	360	365
Leu Ala Asn Asn Ser	Leu Arg Gly Val Ile Pro	Ser Phe Gly Leu Met
370	375	380
Thr Asp Leu Arg Val	Val Met Leu Tyr Ser Asn	Gln Leu Glu Ala Gly
385	390	395
Asp Trp Ala Phe Leu	Ser Ser Leu Lys Asn Cys	Ser Asn Leu Gln Lys
405	410	415
Leu His Phe Gly Glu	Asn Asn Leu Arg Gly Asp	Met Pro Ser Ser Val
420	425	430
Ala Glu Leu Pro Lys	Thr Leu Thr Ser Leu Ala	Leu Pro Ser Asn Tyr
435	440	445
Ile Ser Gly Thr Ile	Pro Leu Glu Ile Gly Asn	Leu Ser Ser Ile Ser
450	455	460
Leu Leu Tyr Leu Gly	Asn Asn Leu Leu Thr Gly	Ser Ile Pro His Thr
465	470	475
Leu Gly Gln Leu Asn	Asn Leu Val Val Leu Ser	Leu Ser Gln Asn Ile
485	490	495
Phe Ser Gly Glu Ile	Pro Gln Ser Ile Gly Asn	Leu Asn Arg Leu Thr
500	505	510
Glu Leu Tyr Leu Ala	Glu Asn Gln Leu Thr Gly	Arg Ile Pro Ala Thr
515	520	525
Leu Ser Arg Cys Gln	Gln Leu Ala Leu Asn Leu	Ser Cys Asn Ala
530	535	540
Leu Thr Gly Ser Ile	Ser Gly Asp Met Phe Ile	Lys Leu Asn Gln Leu
545	550	555
Ser Trp Leu Leu Asp	Leu Ser His Asn Gln Phe	Ile Asn Ser Ile Pro
565	570	575
Leu Glu Leu Gly Ser	Leu Ile Asn Leu Ala Ser	Leu Asn Ile Ser His
580	585	590
Asn Lys Leu Thr Gly	Arg Ile Pro Ser Thr Leu	Gly Ser Cys Val Arg
595	600	605
Leu Glu Ser Leu Arg	Val Gly Gly Asn Phe Leu	Glu Gly Ser Ile Pro
610	615	620
Gln Ser Leu Ala Asn	Leu Arg Gly Thr Lys Val	Leu Asp Phe Ser Gln
625	630	635
Asn Asn Leu Ser Gly	Ala Ile Pro Asp Phe Phe	Gly Thr Phe Thr Ser
645	650	655
Leu Gln Tyr Leu Asn	Met Ser Tyr Asn Phe Glu	Gly Pro Ile Pro
660	665	670
Val Asp Gly Ile Phe	Ala Asp Arg Asn Lys Val	Phe Val Gln Gly Asn
675	680	685
Pro His Leu Cys Thr	Asn Val Pro Met Asp Glu	Leu Thr Val Cys Ser
690	695	700
Ala Ser Ala Ser Lys	Arg Lys Asn Lys Leu Ile	Pro Met Leu Ala
705	710	715
		720

20010-04USA.ST25.txt

Ala Phe Ser Ser Ile Ile Leu Leu Ser Ser Ile Leu Gly Leu Tyr Phe
 725 730 735
 Leu Ile Val Asn Val Phe Leu Lys Arg Lys Trp Lys Ser Asn Glu His
 740 745 750
 Met Asp His Thr Tyr Met Glu Leu Lys Thr Leu Thr Tyr Ser Asp Val
 755 760 765
 Ser Lys Ala Thr Asn Asn Phe Ser Ala Ala Asn Ile Val Gly Ser Gly
 770 775 780
 His Phe Gly Thr Val Tyr Arg Gly Ile Leu His Thr Glu Asp Thr Met
 785 790 795 800
 Val Ala Val Lys Val Phe Lys Leu Asp Gln Cys Gly Ala Leu Asp Ser
 805 810 815
 Phe Met Ala Glu Cys Lys Ala Leu Lys Asn Ile Arg His Arg Asn Leu
 820 825 830
 Val Lys Val Ile Thr Ala Cys Ser Thr Tyr Asp Pro Met Gly Ser Glu
 835 840 845
 Phe Lys Ala Leu Val Phe Glu Tyr Met Ala Asn Gly Ser Leu Glu Ser
 850 855 860
 Arg Leu His Thr Lys Phe Asp Arg Cys Gly Asp Leu Ser Leu Gly Glu
 865 870 875 880
 Arg Ile Ser Ile Ala Phe Asp Ile Ala Ser Ala Leu Glu Tyr Leu His
 885 890 895
 Asn Gln Cys Ile Pro Pro Val Val His Cys Asp Leu Lys Pro Ser Asn
 900 905 910
 Val Leu Phe Asn Asn Asp Asp Val Ala Cys Val Cys Asp Phe Gly Leu
 915 920 925
 Ala Arg Ser Ile Arg Val Tyr Ser Ser Gly Thr Gln Ser Ile Ser Thr
 930 935 940
 Ser Met Ala Gly Pro Arg Gly Ser Ile Gly Tyr Ile Ala Pro Glu Tyr
 945 950 955 960
 Gly Met Gly Ser Gln Ile Ser Thr Glu Gly Asp Val Tyr Ser Tyr Gly
 965 970 975
 Ile Ile Leu Leu Glu Met Leu Thr Gly Arg His Pro Thr Asn Glu Ile
 980 985 990
 Phe Thr Asp Gly Leu Thr Leu Arg Met Tyr Val Asn Ala Ser Leu Ser
 995 1000 1005
 Gln Ile Lys Asp Ile Leu Asp Pro Arg Leu Ile Pro Glu Met Thr Glu
 1010 1015 1020
 Gln Pro Ser Asn His Thr Leu Gln Leu His Glu His Lys Lys Thr Val
 1025 1030 1035 1040
 Pro Ser Arg Cys Lys Leu Gly Gly Val Glu Gly Ile Leu Thr Cys Thr
 1045 1050 1055
 Ile Arg Glu Ile Ala Ser Lys Leu Gly Gly Leu Arg Leu Ser Met Leu
 1060 1065 1070
 Thr

<210> 55

<211> 637

<212> PRT

<213> Oryza sativa

<220>

<221> PEPTIDE

<222> (0)...(0)

<223> line 1B-207-27 polypeptide sequence

<400> 55

Met Gln Asp His Ile Leu Thr Ala Phe Leu Val Val Ser Leu Leu Phe
 1 5 10 15
 Ala Cys Ile Pro Pro Ala Lys Ser Ala Asp Leu Asn Ser Asp Lys Gln
 20 25 30

20010-04USA.ST25.txt

Ala Leu Leu Ala Phe Ala Ala Ser Leu Pro His Gly Arg Lys Leu Asn
 35 40 45
 Trp Ser Ser Ala Ala Pro Val Cys Thr Ser Trp Val Gly Val Thr Cys
 50 55 60
 Thr Pro Asp Asn Ser Arg Val Gln Thr Leu Arg Leu Pro Ala Val Gly
 65 70 75 80
 Leu Phe Gly Pro Leu Pro Ser Asp Thr Leu Gly Lys Leu Asp Ala Leu
 85 90 95
 Glu Val Leu Ser Leu Arg Ser Asn Arg Ile Thr Val Asp Leu Pro Pro
 100 105 110
 Glu Val Gly Ser Ile Pro Ser Leu His Ser Leu Tyr Leu Gln His Asn
 115 120 125
 Asn Leu Ser Gly Ile Ile Pro Thr Ser Leu Thr Ser Thr Leu Thr Phe
 130 135 140
 Leu Asp Leu Ser Tyr Asn Thr Phe Asp Gly Glu Ile Pro Leu Arg Val
 145 150 155 160
 Gln Asn Leu Thr Gln Leu Thr Ala Leu Leu Leu Gln Asn Asn Ser Leu
 165 170 175
 Ser Gly Pro Ile Pro Asp Leu Gln Leu Pro Lys Leu Arg His Leu Asn
 180 185 190
 Leu Ser Asn Asn Asn Leu Ser Gly Pro Ile Pro Pro Ser Leu Gln Arg
 195 200 205
 Phe Pro Ala Asn Ser Phe Leu Gly Asn Ala Phe Leu Cys Gly Phe Pro
 210 215 220
 Leu Gln Pro Cys Pro Gly Thr Ala Pro Ser Pro Ser Pro Ser Pro Thr
 225 230 235 240
 Ser Pro Ser Pro Gly Lys Ala Lys Lys Gly Phe Trp Lys Arg Ile Arg
 245 250 255
 Thr Gly Val Ile Ile Ala Leu Ala Ala Ala Gly Gly Val Leu Leu Leu
 260 265 270
 Ile Leu Ile Val Leu Leu Leu Ile Cys Ile Phe Lys Arg Lys Lys Ser
 275 280 285
 Thr Glu Pro Thr Thr Ala Ser Ser Ser Lys Gly Lys Thr Val Ala Gly
 290 295 300
 Gly Arg Gly Glu Asn Pro Lys Glu Glu Tyr Ser Ser Gly Val Gln Glu
 305 310 315 320
 Ala Glu Arg Asn Lys Leu Val Phe Phe Glu Gly Cys Ser Tyr Asn Phe
 325 330 335
 Asp Leu Glu Asp Leu Leu Arg Ala Ser Ala Glu Val Leu Gly Lys Gly
 340 345 350
 Ser Tyr Gly Thr Thr Tyr Lys Ala Val Leu Glu Asp Gly Thr Thr Val
 355 360 365
 Val Val Lys Arg Leu Lys Glu Val Val Val Gly Lys Lys Asp Phe Glu
 370 375 380
 Gln Gln Met Glu Ile Val Gly Arg Val Gly Gln His Gln Asn Val Val
 385 390 395 400
 Pro Leu Arg Ala Tyr Tyr Tyr Ser Lys Asp Glu Lys Leu Leu Val Tyr
 405 410 415
 Asp Tyr Ile Pro Ser Gly Ser Leu Ala Val Val Leu His Gly Asn Lys
 420 425 430
 Ala Thr Gly Lys Ala Pro Leu Asp Trp Glu Thr Arg Val Lys Ile Ser
 435 440 445
 Leu Gly Val Ala Arg Gly Ile Ala His Leu His Ala Glu Gly Gly Gly
 450 455 460
 Lys Phe Ile His Gly Asn Leu Lys Ser Ser Asn Ile Leu Leu Ser Gln
 465 470 475 480
 Asn Leu Asp Gly Cys Val Ser Glu Phe Gly Leu Ala Gln Leu Met Thr
 485 490 495
 Ile Pro Pro Ala Pro Ala Arg Leu Val Gly Tyr Arg Ala Pro Glu Val
 500 505 510
 Leu Glu Thr Lys Lys Pro Thr Gln Lys Ser Asp Val Tyr Ser Phe Gly
 515 520 525
 Val Leu Val Leu Glu Met Leu Thr Gly Lys Ala Pro Leu Arg Ser Pro

20010-04USA.ST25.txt

530		535		540
Gly	Arg	Glu	Asp	Ser
545		550		555
Val	Arg	Glu	Glu	Trp
		565		570
His	Pro	Asn	Ile	Glu
		580		585
Ala	Cys	Val	Ala	Ala
		595		600
Ile	Arg	Arg	Ile	Val
		610		615
Pro	Pro	Glu	Glu	Lys
625				630
				635

<210> 56
 <211> 523
 <212> PRT
 <213> Oryza sativa

<220>
 <221> PEPTIDE
 <222> (0)...(0)
 <223> line 1B-138-07 polypeptide sequence

<400> 56

Met	Ala	Ala	Pro	Leu	Ser	Thr	Ala	Ala	Ala	Ala	Ser	Trp	Leu	Ser	Asp
1				5					10				15		
Ser	Ala	Ser	Ser	Pro	Pro	Arg	Val	Arg	Leu	Leu	Ile	Gly	Gly	Glu	Phe
			20					25					30		
Val	Glu	Ser	Arg	Ala	Asp	Glu	His	Val	Asp	Val	Thr	Asn	Pro	Ala	Thr
		35					40					45			
Gln	Glu	Val	Val	Ser	Arg	Ile	Pro	Leu	Thr	Thr	Ala	Asp	Glu	Phe	Arg
		50				55					60				
Ala	Ala	Val	Asp	Ala	Ala	Arg	Thr	Ala	Phe	Pro	Gly	Trp	Arg	Asn	Thr
65				70					75					80	
Pro	Val	Thr	Thr	Arg	Gln	Arg	Ile	Met	Leu	Lys	Tyr	Gln	Glu	Leu	Ile
				85				90						95	
Arg	Ala	Asn	Met	Asp	Lys	Leu	Ala	Glu	Asn	Ile	Thr	Thr	Glu	Gln	Gly
			100					105					110		
Lys	Thr	Leu	Lys	Asp	Ala	Trp	Gly	Asp	Val	Phe	Arg	Gly	Leu	Glu	Val
		115					120					125			
Val	Glu	His	Ala	Cys	Gly	Met	Gly	Thr	Leu	Gln	Met	Gly	Glu	Tyr	Val
		130				135					140				
Ser	Asn	Val	Ser	Asn	Gly	Ile	Asp	Thr	Phe	Ser	Ile	Arg	Glu	Pro	Leu
145					150				155					160	
Gly	Val	Cys	Ala	Gly	Ile	Cys	Pro	Phe	Asn	Phe	Pro	Ala	Met	Ile	Pro
				165				170						175	
Leu	Trp	Met	Phe	Pro	Ile	Ala	Val	Thr	Cys	Gly	Asn	Thr	Phe	Val	Leu
			180					185					190		
Lys	Pro	Ser	Glu	Lys	Asp	Pro	Gly	Ala	Ala	Met	Met	Leu	Ala	Glu	Leu
		195					200					205			
Ala	Met	Glu	Ala	Gly	Leu	Pro	Lys	Gly	Val	Leu	Asn	Ile	Val	His	Gly
		210				215					220				
Thr	His	Asp	Val	Val	Asn	Asn	Ile	Cys	Asp	Asp	Glu	Asp	Ile	Lys	Ala
225					230				235					240	
Val	Ser	Phe	Val	Gly	Ser	Asn	Ile	Ala	Gly	Met	His	Ile	Tyr	Ser	Arg
				245					250					255	
Ala	Ser	Ala	Lys	Gly	Lys	Arg	Val	Gln	Ser	Asn	Met	Gly	Ala	Lys	Asn
			260					265					270		
His	Ala	Ile	Ile	Leu	Pro	Asp	Ala	Asp	Arg	Asp	Ala	Thr	Leu	Asn	Ala
		275					280					285			
Leu	Ile	Ala	Ala	Gly	Phe	Gly	Ala	Ala	Gly	Gln	Arg	Cys	Met	Ala	Leu

20010-04USA.ST25.txt

290	Ser Thr Ala Val Phe Val Gly Gly Ser Glu Pro Trp Ile Arg Pro Gly	295	300
305	Ile Arg Glu Asp Glu Leu Val Lys Arg Ala Ser Ser Leu Val Val Asn	310	320
		325	335
	Ser Gly Met Ala Ser Asp Ala Asp Leu Gly Pro Val Ile Ser Lys Gln	340	350
	Ala Lys Glu Arg Ile Cys Lys Leu Ile Gln Ser Gly Ala Asp Asn Gly	355	365
	Ala Arg Val Leu Leu Asp Gly Arg Asp Ile Val Val Pro Asn Phe Glu	370	380
	Asn Gly Asn Phe Val Gly Pro Thr Leu Leu Ala Asp Val Lys Ser Glu	385	400
	Met Glu Cys Tyr Lys Glu Glu Ile Phe Gly Pro Val Leu Leu Leu Met	405	415
	Lys Ala Glu Ser Leu Asp Asp Ala Ile Gln Ile Val Asn Arg Asn Lys	420	430
	Tyr Gly Asn Gly Ala Ser Ile Phe Thr Thr Ser Gly Val Ser Ala Arg	435	445
	Lys Phe Gln Thr Asp Ile Glu Ala Gly Gln Val Gly Ile Asn Val Pro	450	460
	Ile Pro Val Pro Leu Pro Phe Phe Ser Phe Thr Gly Ser Lys Ala Ser	465	480
	Phe Ala Gly Asp Leu Asn Phe Tyr Gly Lys Ala Gly Val Gln Phe Phe	485	495
	Thr Gln Ile Lys Thr Val Thr Gln Gln Trp Lys Glu Ser Pro Ala Gln	500	510
	Arg Val Ser Leu Ser Met Pro Thr Ser Gln Lys	515	520

<210> 57

<211> 446

<212> PRT

<213> Oryza sativa

<220>

<221> PEPTIDE

<222> (0)...(0)

<223> line 1D-059-12 polypeptide sequence

<400> 57

Met Ala Ala Ala Ala Thr Ala Ala Val Pro Leu Asp Glu Ala Lys Ala	1	5	10	15
Lys Glu Val Leu Arg Gln Val Glu Phe Tyr Phe Ser Asp Ser Asn Leu	20	25	30	
Pro Arg Asp Asn Phe Leu Arg Lys Thr Val Glu Glu Ser Glu Asp Gly	35	40	45	
Leu Val Ser Leu Ala Leu Ile Cys Ser Phe Ser Arg Met Lys Lys His	50	55	60	
Leu Gly Leu Asp Ala Asp Val Lys Gln Glu Thr Met Pro Glu Glu Thr	65	70	75	80
Val Leu Ala Val Ala Glu Val Leu Arg Arg Ser Ser Ala Leu Arg Val	85	90	95	
Thr Glu Asp Gly Lys Lys Val Gly Arg Ser Ile Glu Leu Ser Lys Leu	100	105	110	
Asp Glu Ile Met Glu Gln Val Asp Ser Arg Thr Ile Ala Ala Ser Pro	115	120	125	
Phe Pro Tyr Asn Val Lys Leu Glu Asp Val Gln Ser Phe Phe Ala Gln	130	135	140	
Tyr Gly Lys Val Asn Ser Val Arg Leu Pro Arg His Ile Ala Asp Lys	145	150	155	160
Arg His Phe Cys Gly Thr Ala Leu Val Glu Phe Ser Glu Glu Glu Glu				

20010-04USA.ST25.txt

Ala	Asn	Ala	Val	165	Leu	Lys	Asn	Thr	Leu	170	Val	Phe	Ala	Gly	Ala	175	Asp	Leu
Glu	Ile	Lys	Pro	180	Lys	Lys	Glu	Phe	185	Asp	Thr	Glu	Arg	Glu	190	Ala	Lys	Lys
Glu	Ala	Tyr	Glu	195	Lys	Ser	Gln	Pro	200	Thr	Lys	Asn	Gly	His	205	Asp	Glu	Gly
Tyr	Pro	Lys	Gly	210	Leu	Ile	Val	Ala	215	Phe	Lys	Leu	Lys	Ile	Ile	Gln	Ile	
225	Asp	Gly	Gly	Met	230	Ala	Asn	Gly	Gly	235	Lys	Glu	Gly	Glu	Thr	Asp		
Asp	Ala	Asn	Lys	245	Ser	Arg	Thr	Gly	His	250	Asp	Glu	Lys	Ile	Pro	Glu	Asn	
Ser	Asp	Ile	Lys	260	Glu	Asp	Leu	Ser	265	Asp	Asp	Val	Glu	Lys	Ser	Lys	Glu	
Ala	Ala	Ala	Gln	275	Ser	Val	Lys	Lys	280	Gly	Glu	Ser	Pro	Ser	Glu	Asn	Ala	
Asp	Asp	Pro	Ile	290	Ser	Arg	Glu	Asp	295	Phe	Lys	Glu	Glu	Phe	Gly	Lys	Phe	
305	Gly	Thr	Val	Arg	310	Val	Asp	Phe	Ser	315	Ile	Gly	Glu	Asp	Ser	Gly	Tyr	
Ile	Arg	Phe	Glu	325	Asp	Ser	Lys	Ala	330	Glu	Lys	Ala	Arg	Ala	Leu	Ala		
Ala	Ile	Ser	Asp	340	Glu	Gly	Gly	Leu	345	Ile	Met	Lys	Gly	His	Leu	Val	Thr	
Leu	Glu	Pro	Val	355	Ser	Gly	Gln	Ala	360	Glu	Lys	Asp	Tyr	Trp	Ser	Ala	Ile	
Lys	Gly	Gly	Gln	370	Gly	Lys	Tyr	Arg	375	Asp	Asn	Arg	Ser	Asn	Arg	Gly	Arg	
385	Ala	Asp	Pro	Leu	390	Tyr	His	Asn	400	Ala	Pro	Arg	Met	Asn	Leu	Arg	Ser	
Gly	Leu	Lys	Leu	405	Lys	Ile	Glu	Val	410	Ala	Leu	Trp	His	Thr	Arg	Met		
Pro	Thr	His	Ile	420	Phe	Gly	Val	Ile	425	Leu	Ser	Trp	Asn	Trp	Gln			
		435						440						445				

<210> 58

<211> 859

<212> PRT

<213> Oryza sativa

<220>

<221> PEPTIDE

<222> (0)...(0)

<223> line 1C-087-40 polypeptide sequence

<400> 58

Met	Ala	Thr	Arg	Tyr	Trp	Ile	Val	Ser	Leu	Pro	Val	Gln	Thr	Pro	Gly
1				5					10					15	
Ser	Thr	Ala	Asn	Ser	Leu	Trp	Ala	Arg	Leu	Gln	Asp	Ser	Ile	Ser	Arg
			20					25					30		
His	Ser	Phe	Asp	Thr	Pro	Leu	Tyr	Arg	Phe	Asn	Val	Pro	Asp	Leu	Arg
		35					40					45			
Val	Gly	Thr	Leu	Asp	Ser	Leu	Leu	Ala	Leu	Ser	Asp	Asp	Leu	Val	Lys
	50					55					60				
Ser	Asn	Val	Phe	Ile	Glu	Gly	Val	Ser	His	Lys	Ile	Arg	Arg	Gln	Ile
65					70				75					80	
Glu	Glu	Leu	Glu	Arg	Ala	Gly	Gly	Val	Glu	Ser	Gly	Ala	Leu	Thr	Val
				85					90					95	
Asp	Gly	Val	Pro	Val	Asp	Thr	Tyr	Leu	Thr	Arg	Phe	Val	Trp	Asp	Glu
			100					105					110		
Gly	Lys	Tyr	Pro	Thr	Met	Ser	Pro	Leu	Lys	Glu	Ile	Val	Gly	Ser	Ile

20010-0405A.15725.txt															
115															
Gln	Ser	Gln	Val	Ser	Lys	Ile	Glu	Asp	Asp	Met	Lys	Val	Arg	Gly	Ala
Glu	Tyr	Asn	Asn	Val	Arg	Ser	Gln	Leu	Ser	Ala	Ile	Asn	Arg	Lys	Gln
145					150					155					160
Thr	Gly	Ser	Leu	Ala	Val	Arg	Asp	Leu	Ser	Asn	Leu	Val	Lys	Pro	Glu
				165						170					
Asp	Met	Val	Thr	Ser	Glu	His	Leu	Val	Thr	Leu	Leu	Ala	Val	Val	Pro
			180										190		
Lys	Tyr	Ser	Gln	Lys	Asp	Trp	Leu	Ser	Ser	Tyr	Glu	Ser	Leu	Asp	Thr
		195					200					205			
Phe	Val	Val	Pro	Arg	Ser	Ser	Lys	Lys	Leu	Tyr	Glu	Asp	Asn	Glu	Tyr
	210					215					220				
Ala	Leu	Tyr	Thr	Val	Thr	Leu	Phe	Ala	Lys	Val	Val	Asp	Asn	Phe	Lys
225					230					235					240
Val	Arg	Ala	Arg	Glu	Lys	Gly	Phe	Gln	Val	Arg	Asp	Phe	Glu	Tyr	Ser
				245										255	
Ser	Glu	Ala	Gln	Glu	Ser	Arg	Lys	Glu	Glu	Leu	Glu	Lys	Leu	Met	Gln
			260										270		
Asp	Gln	Glu	Ala	Met	Arg	Ala	Ser	Leu	Leu	Gln	Trp	Cys	Tyr	Ala	Ser
		275					280					285			
Tyr	Ser	Glu	Asn	Thr	Ile	Tyr	Val	Arg	His	Ala	Lys	Val	Gln	Asn	Phe
		290				295					300				
Val	Leu	Leu	Tyr	Val	Phe	Ser	Ser	Trp	Met	His	Phe	Cys	Ala	Val	Arg
305					310					315					320
Val	Phe	Val	Glu	Ser	Ile	Leu	Arg	Tyr	Gly	Leu	Pro	Pro	Ser	Phe	Leu
				325					330					335	
Ser	Ala	Val	Leu	Ala	Pro	Ser	Gln	Lys	Gly	Glu	Lys	Lys	Val	Arg	Ser
			340										350		
Ile	Leu	Glu	Glu	Leu	Cys	Gly	Asn	Val	His	Ser	Ile	Tyr	Trp	Lys	Ser
		355					360					365			
Glu	Asp	Asp	Val	Gly	Val	Ala	Gly	Leu	Gly	Glu	His	Arg	Val	Arg	Cys
	370					375					380				
Cys	Gly	Tyr	Tyr	Val	Phe	Val	Thr	Leu	Ser	Ser	Gln	Lys	Asp	Lys	Leu
385					390					395					400
Gly	Val	Met	Tyr	Arg	Thr	Ser	Ile	Leu	Gly	Asp	Pro	Val	Pro	Thr	Asp
				405					410					415	
Asp	Ser	Arg	Val	Asp	Lys	Thr	Gln	Glu	Glu	Met	Met	Val	Lys	Glu	Lys
			420					425					430		
Glu	Ile	His	Val	Met	Ser	Asn	Arg	Arg	Lys	Arg	Gly	Glu	Ser	Lys	
		435					440				445				
Pro	Gln	Ala	His	Asp	Ala	Gly	Asp	Thr	Thr	Pro	Ile	Asp	Asn	Ile	Leu
	450					455					460				
Thr	Ser	Leu	Asp	Asp	Ala	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Arg	Arg	Glu
465					470					475					480
Leu	Pro	Leu	Leu	Gln	Leu	Asn	Asp	His	Gln	Glu	Ala				

20010-04USA.ST25.txt

Thr	Ser	Thr	Ala	Tyr	Lys	Thr	Arg	Phe	Glu	Ala	Thr	Ser	Gly	Val	Ser
625					630					635					640
Gly	Val	Val	Gly	Ala	Met	Tyr	Thr	Thr	His	Ile	Pro	Ile	Ile	Ala	Pro
				645					650					655	
Lys	Val	Ser	Val	Ala	Ala	Tyr	Leu	Asn	Arg	Arg	His	Thr	Glu	Arg	Asn
			660					665					670		
His	Lys	Thr	Ser	Tyr	Ser	Ile	Thr	Leu	Gln	Gly	Val	Val	Gly	Pro	Asp
		675					680					685			
Gly	Thr	Phe	Thr	Asp	Val	Cys	Ile	Gly	Trp	Pro	Gly	Ser	Met	Ser	Asp
		690				695					700				
Glu	Gln	Val	Leu	Arg	Lys	Ser	Ala	Leu	His	Gln	Arg	Ala	Ser	Ala	Ala
705					710					715					720
Ala	Gly	Ser	Met	Ser	Trp	Val	Val	Gly	Gly	Ala	Ser	Tyr	Pro	Leu	Thr
				725					730					735	
Glu	Trp	Met	Leu	Val	Pro	Tyr	Ala	Gln	Arg	Asn	Leu	Thr	Trp	Thr	Gln
			740					745					750		
His	Ala	Phe	Asn	Glu	Lys	Val	Gly	Glu	Val	Arg	Arg	Val	Ala	Thr	Glu
		755					760					765			
Ala	Phe	Val	Arg	Leu	Lys	Gly	Arg	Trp	Ala	Cys	Leu	Gln	Lys	Arg	Thr
	770					775				780					
Glu	Val	Lys	Leu	Gln	Asp	Leu	Pro	Ala	Val	Leu	Ala	Ala	Cys	Cys	Val
785					790					795					800
Leu	His	Asn	Ile	Cys	Glu	Thr	Arg	Gly	Glu	Asp	Met	Asp	Pro	Asp	Leu
				805					810					815	
Arg	Cys	Asp	Leu	Pro	Pro	Asp	Glu	Glu	Glu	Asp	Asp	Thr	Val	Leu	Val
			820					825					830		
Gln	Ser	Glu	Ser	Ala	Asn	Lys	Val	Arg	Asp	Asp	Ile	Ala	His	Asn	Leu
		835					840					845			
Leu	His	Arg	Gly	Leu	Ala	Gly	Thr	Ala	Phe	Phe					
	850					855									

<210> 59

<211> 473

<212> PRT

<213> Oryza sativa

<220>

<221> PEPTIDE

<222> (0)...(0)

<223> line 1C-017-14 polypeptide sequence

<400> 59

Met	Asp	Ala	Leu	Leu	Val	Glu	Lys	Val	Leu	Leu	Gly	Leu	Phe	Val	Ala
1				5					10					15	
Ala	Val	Leu	Ala	Leu	Val	Val	Ala	Lys	Leu	Thr	Gly	Lys	Arg	Leu	Arg
			20					25					30		
Leu	Pro	Pro	Gly	Pro	Ala	Gly	Ala	Pro	Ile	Val	Gly	Asn	Trp	Leu	Gln
		35					40					45			
Val	Gly	Asp	Asp	Leu	Asn	His	Arg	Asn	Leu	Met	Ala	Leu	Ala	Arg	Arg
	50					55					60				
Phe	Gly	Asp	Ile	Leu	Leu	Leu	Arg	Met	Gly	Val	Arg	Asn	Leu	Val	Val
65				70						75					80
Val	Ser	Ser	Pro	Asp	Leu	Ala	Lys	Glu	Val	Leu	His	Thr	Gln	Gly	Val
				85					90					95	
Glu	Phe	Gly	Ser	Arg	Thr	Arg	Asn	Val	Val	Phe	Asp	Ile	Phe	Thr	Gly
			100					105					110		
Lys	Gly	Gln	Asp	Met	Val	Phe	Thr	Val	Tyr	Gly	Asp	His	Trp	Arg	Lys
		115					120					125			
Met	Arg	Arg	Ile	Met	Thr	Val	Pro	Phe	Phe	Thr	Asn	Lys	Val	Val	Ala
	130					135					140				
Gln	Asn	Arg	Ala	Gly	Trp	Glu	Glu	Glu	Ala	Arg	Leu	Val	Val	Glu	Asp
145					150					155					160

20010-04USA.ST25.txt

Val Arg Arg Asp Pro Thr Ala Ala Thr Ser Gly Val Val Ile Arg Arg
 165 170 175
 Arg Leu Gln Leu Met Met Tyr Asn Asp Met Phe Arg Ile Met Phe Asp
 180 185 190
 Arg Arg Phe Asp Ser Val Asp Asp Pro Leu Phe Asn Lys Leu Lys Ala
 195 200 205
 Phe Asn Ala Glu Arg Ser Arg Leu Ser Gln Ser Phe Glu Tyr Asn Tyr
 210 215 220
 Gly Asp Phe Ile Pro Val Leu Arg Pro Phe Leu Arg Arg Tyr Leu Ala
 225 230 235 240
 Arg Cys His Gln Leu Lys Ser Gln Arg Met Lys Leu Phe Glu Asp His
 245 250 255
 Phe Val Gln Glu Arg Lys Arg Val Met Glu Gln Thr Gly Glu Ile Arg
 260 265 270
 Cys Ala Met Asp His Ile Leu Glu Ala Glu Arg Lys Gly Glu Ile Asn
 275 280 285
 His Asp Asn Val Leu Tyr Ile Val Glu Asn Ile Asn Val Ala Ala Ile
 290 295 300
 Glu Thr Thr Leu Trp Ser Ile Glu Trp Gly Ile Ala Glu Leu Val Asn
 305 310 315 320
 His Pro Ser Ile Gln Ser Lys Val Arg Glu Glu Met Ala Ser Val Leu
 325 330 335
 Gly Gly Ala Ala Val Thr Glu Pro Asp Leu Glu Arg Leu Pro Tyr Leu
 340 345 350
 Gln Ala Val Val Lys Glu Thr Leu Arg Leu Arg Met Ala Ile Pro Leu
 355 360 365
 Leu Val Pro His Met Asn Leu Ala Asp Gly Lys Leu Ala Gly Tyr Asp
 370 375 380
 Ile Pro Ala Glu Ser Lys Ile Leu Val Asn Ala Trp Phe Leu Ala Asn
 385 390 395 400
 Asp Pro Lys Arg Trp Val Arg Pro Asp Glu Phe Arg Pro Glu Arg Phe
 405 410 415
 Leu Glu Glu Glu Lys Ala Val Glu Ala His Gly Asn Asp Phe Arg Phe
 420 425 430
 Val Pro Phe Gly Val Gly Arg Arg Ser Cys Pro Gly Ile Ile Leu Ala
 435 440 445
 Leu Pro Ile Ile Gly Ile Thr Leu Gly Arg Leu Val Gln Ser Phe Asp
 450 455 460
 Leu Leu Pro Pro Pro Gly Met Asp Lys
 465 470

<210> 60

<211> 408

<212> PRT

<213> Oryza sativa

<220>

<221> PEPTIDE

<222> (0)...(0)

<223> line 1C-038-56 polypeptide sequence

<400> 60

Asp Val Gln Gln His Ser Gly Ser Ser Ser Ser Ser Thr Glu Ser Asp
 1 5 10 15
 Val Gln Glu Thr Ala Ala Val Ala Val Ala Asp Pro Ser Pro Arg Ser
 20 25 30
 Glu Val Val Asp Gly Glu Ser Pro Gln Pro Gly Gly Glu Ala Ala
 35 40 45
 Ser His Gln Gln Gln Gln Lys Glu Met Lys Leu Lys Lys Pro Asp Lys
 50 55 60
 Ile Leu Pro Cys Pro Arg Cys Ser Ser Met Asp Thr Lys Phe Cys Tyr
 65 70 75 80

20010-04USA.ST25.txt

Phe Asn Asn Tyr Asn Val Asn Gln Pro Arg His Phe Cys Lys His Cys
 85 90 95
 Gln Arg Tyr Trp Thr Ala Gly Gly Ala Met Arg Asn Val Pro Val Gly
 100 105 110
 Ala Gly Arg Arg Lys Asn Lys Asn Ala Thr Ala Ala Ala His Phe Leu
 115 120 125
 His Arg Val Arg Ala Cys Ala Ala Ala Ala Met Pro Ala Ala Pro
 130 135 140
 His Asp Ala Thr Asn Ala Thr Val Leu Ser Phe Gly Gly Gly Gly Gly
 145 150 155 160
 Gly His Asp Ala Leu Pro Val Thr Leu Asp Leu Ala Asp Lys Met Thr
 165 170 175
 Arg Leu Gly Lys Glu Gly Leu Val Ala His Ala Arg Asn Ala Asp Ala
 180 185 190
 Ala Ala Ala Cys Ser Glu Val Ser Ser Asn Arg Asp Asp Glu Gln Ile
 195 200 205
 Gly Asn Thr Val Ala Lys Pro Ala Asn Gly Leu Gln His Pro Pro
 210 215 220
 Pro Pro His His His His His Ser Ala Met Asn Gly Gly Gly Ile Trp
 225 230 235 240
 Pro Tyr Tyr Thr Ser Gly Ile Ala Ile Pro Ile Tyr Pro Ala Ala Pro
 245 250 255
 Ala Tyr Trp Gly Cys Met Ile Pro Pro Pro Gly Ala Trp Ser Leu Pro
 260 265 270
 Trp Pro Ala Thr Val Gln Ser Gln Ala Ile Ser Ser Ser Ser Pro Pro
 275 280 285
 Thr Ser Ala Thr Pro Ser Val Ser Ser Phe Thr Leu Gly Lys His Pro
 290 295 300
 Arg Glu Gly Gly Asp His Glu Ala Arg Asp His His Gly Asn Gly Lys
 305 310 315 320
 Val Trp Val Pro Lys Thr Ile Arg Ile Asp Asn Ala Asp Glu Val Ala
 325 330 335
 Arg Ser Ser Ile Arg Ser Leu Phe Ala Phe Arg Gly Gly Asp Lys Val
 340 345 350
 Asp Asp Asn Asn Asp Asp Asp Gly Thr Ser Val His Lys Leu Ala Thr
 355 360 365
 Thr Val Phe Glu Pro Lys Arg Asp Gly Lys Thr Ala Lys His Pro Ala
 370 375 380
 Ile Thr Ser Leu Pro Leu Leu His Thr Asn Pro Val Ala Leu Thr Arg
 385 390 395 400
 Ser Ala Thr Phe Gln Glu Gly Ser
 405

<210> 61

<211> 290

<212> PRT

<213> Oryza sativa

<220>

<221> PEPTIDE

<222> (O)...(O)

<223> line 1C-041-47 polypeptide sequence

<400> 61

Met Gly Ile Lys Gly Leu Thr Lys Leu Leu Ala Asp Asn Ala Pro Lys
 1 5 10 15
 Ala Met Lys Glu Gln Lys Phe Glu Ser Tyr Phe Gly Arg Arg Ile Ala
 20 25 30
 Val Asp Ala Ser Met Ser Ile Tyr Gln Phe Leu Ser Phe Ala Arg Tyr
 35 40 45
 Ser Lys Arg Glu Asp Ala Thr Lys Glu Leu Thr Glu Ala Val Glu Glu
 50 55 60

20010-04USA.ST25.txt

Gly Asp Lys Asp Ala Ile Glu Lys Phe Ser Lys Arg Thr Val Lys Val
65 70 75 80
Thr Lys Gln His Asn Glu Glu Cys Lys Arg Leu Leu Arg Leu Met Gly
85 90 95
Val Pro Val Val Glu Val Tyr Ala Val Ala Ser Glu Asp Met Asp Ser
100 105 110
Leu Thr Phe Gly Ala Pro Arg Phe Leu Arg His Leu Met Asp Pro Ser
115 120 125
Ser Lys Lys Ile Pro Val Met Glu Phe Glu Val Ala Lys Val Leu Glu
130 135 140
Glu Leu Glu Leu Thr Met Asp Gln Phe Ile Asp Leu Cys Ile Leu Ser
145 150 155 160
Gly Cys Asp Tyr Cys Asp Ser Ile Lys Gly Ile Gly Gly Gln Thr Ala
165 170 175
Leu Lys Leu Ile Arg Gln His Gly Ser Ile Glu Ser Ile Leu Glu Asn
180 185 190
Ile Asn Lys Asp Arg Tyr Gln Ile Pro Glu Asp Trp Pro Tyr Gln Glu
195 200 205
Ala Arg Arg Leu Phe Lys Glu Pro Asn Val Thr Leu Asp Ile Pro Glu
210 215 220
Leu Lys Trp Asn Ala Pro Asp Glu Glu Ala Ile Glu Lys Ile Lys Phe
225 230 235 240
Ala Lys Asn Lys Ser Ser Gln Gly Arg Leu Glu Ser Phe Phe Lys Pro
245 250 255
Val Val Ser Thr Ser Val Pro Leu Lys Arg Lys Asp Thr Ser Glu Lys
260 265 270
Pro Thr Lys Ala Val Ala Asn Lys Lys Thr Lys Gly Ala Gly Gly Lys
275 280 285
Lys Lys
290

<210> 62

<211> 552

<212> PRT

<213> Oryza sativa

<220>

<221> PEPTIDE

<222> (0)...(0)

<223> line 1C-064-20 polypeptide sequence

<400> 62

Met Ala Ser Ala Pro Gly Asp Gly Lys Gln Gly Gly Gly Gly Gly Gly
1 5 10 15
Pro Ala Val Gly Ile Asp Leu Gly Thr Thr Tyr Ser Cys Val Ala Val
20 25 30
Trp Arg His Asp Arg Gly Glu Val Ile Ala Asn Asp Gln Arg Asn Arg
35 40 45
Leu Thr Pro Ser Cys Val Ala Phe Thr Ala Asp Asp Asp Ser Phe
50 55 60
Val Gly Asp Ala Ala Phe Asn Gln Ser Ala Leu Asn Pro Thr Asn Thr
65 70 75 80
Ile Phe Glu Val Lys Arg Leu Ile Gly Arg Arg Phe Ser Asp Asp Ser
85 90 95
Val Gln Lys Asp Ile Lys Leu Trp Pro Phe Lys Val Val Ala Gly Gln
100 105 110
Glu Asp Arg Pro Met Ile Val Val Arg His Glu Gly Glu Arg Gln
115 120 125
Phe Met Pro Glu Glu Ile Ser Ser Met Val Leu Ala Lys Met Arg Glu
130 135 140
Thr Ala Glu Val Tyr Leu Gly Lys Thr Val Thr Lys Ala Val Ile Thr
145 150 155 160

20010-04USA.ST25.txt

Val Pro Val Tyr Phe Asn Asn Ala Gln Arg Gln Ala Thr Met Asp Ala
 165 170 175
 Gly Ala Ile Ala Gly Leu Asn Val Met Arg Ile Ile Asn Glu Pro Thr
 180 185 190
 Ala Ala Ala Leu Ala Tyr Cys Leu Glu Lys Met Pro Val Ser Asn Lys
 195 200 205
 Gly Arg Met Val Leu Val Phe Asp Leu Gly Gly Gly Thr Phe Asp Ile
 210 215 220
 Ser Leu Leu Asn Ile Asp Pro Gly Glu Gly Thr Ala Gly Asp Thr His
 225 230 235 240
 Leu Gly Gly Ala Asp Phe Asp Asn Glu Leu Val Lys His Ser Leu Arg
 245 250 255
 Glu Phe Asn Arg Lys His Gly Ser Met Asp Ile Glu Ser Asn Gln Lys
 260 265 270
 Ala Leu Arg Arg Leu Arg Thr Ala Cys Glu Arg Ala Lys Arg Met Leu
 275 280 285
 Ser Ser Thr Met Gln Thr Thr Ile Glu Val Asp Ser Leu His Gln Gly
 290 295 300
 Ile Asp Phe Arg Val Thr Leu Thr Arg Ser Arg Phe Glu Glu Leu Asn
 305 310 315 320
 Lys Asp Leu Phe Ser Lys Cys Met Glu Ala Met Glu Asn Cys Leu Arg
 325 330 335
 Asp Ala Lys Val Asp Lys Trp Ser Val Asp Asp Val Val Leu Val Gly
 340 345 350
 Gly Ser Thr Arg Ile Pro Lys Val Gln Lys Met Leu Ser Glu Phe Phe
 355 360 365
 Asp Gly Lys Glu Leu Cys Arg Ser Ile Asn Pro Asp Glu Ala Val Ala
 370 375 380
 Tyr Gly Ala Ala Ile Gln Ala Ser Ile Leu Cys Gly Gly Thr Asp Asp
 385 390 395 400
 Lys Arg Leu Val Asp Met Leu Leu Arg Glu Val Thr Pro Leu Ser Leu
 405 410 415
 Gly Val Glu Thr Glu Asp Asn Cys Thr Met Ser Val Val Ile Pro Arg
 420 425 430
 Asn Thr Ala Ile Pro Thr Lys Lys Val Lys Asn Phe Thr Thr Leu Tyr
 435 440 445
 Asp Asn Gln Ile Asn Val Ser Phe Pro Val Tyr Glu Gly Glu Ser Ala
 450 455 460
 Asn Thr Lys Asp Asn Asn Leu Leu Gly Glu Phe Thr Leu Tyr Gly Ile
 465 470 475 480
 Pro Pro Ala Pro Lys Arg Val Pro Ser Ile Asp Val Thr Phe Asp Ile
 485 490 495
 Asp Ala Asn Gly Val Leu Asn Val Ser Ala Glu His Lys Val Thr Gly
 500 505 510
 Gln Lys Asn Ser Ile Thr Ile Thr Asn Arg Ser Gly Arg Leu Asn Gln
 515 520 525
 Glu Glu Ile Asp Arg Met Ala Leu Glu Pro Glu Arg His Lys Met Lys
 530 535 540
 Arg Ile Lys Leu His Glu Val Val
 545 550

<210> 63

<211> 479

<212> PRT

<213> Oryza sativa

<220>

<221> PEPTIDE

<222> (0)...(0)

<223> line 1C-109-35 polypeptide sequence

<400> 63

20010-04USA.ST25.txt

```

Met Ser Ser Ser Ala Thr Val Val Pro Leu Ala Tyr Gln Gly Asn Thr
1      5      10      15
Ser Ala Ser Val Ala Asp Trp Leu Asn Lys Gly Asp Asn Ala Trp Gln
20      25      30
Leu Val Ala Ala Thr Leu Val Gly Leu Gln Ser Val Pro Gly Leu Val
35      40      45
Val Leu Tyr Gly Gly Val Val Lys Lys Lys Trp Ala Val Asn Ser Ala
50      55      60
Phe Met Ala Leu Tyr Ala Phe Ala Ala Val Trp Ile Cys Trp Val Thr
65      70      75      80
Trp Ala Tyr Asn Met Ser Phe Gly Glu Lys Leu Leu Pro Ile Trp Gly
85      90      95
Lys Ala Arg Pro Ala Leu Asp Gln Gly Leu Leu Val Gly Arg Ala Ala
100      105      110
Leu Pro Ala Thr Val His Tyr Arg Ala Asp Gly Ser Val Glu Thr Ala
115      120      125
Ala Val Glu Pro Leu Tyr Pro Met Ala Thr Val Val Tyr Phe Gln Cys
130      135      140
Val Phe Ala Ala Ile Thr Leu Ile Leu Val Ala Gly Ser Leu Leu Gly
145      150      155      160
Arg Met Ser Phe Leu Ala Trp Met Ile Phe Val Pro Leu Trp Leu Thr
165      170      175
Phe Ser Tyr Thr Val Gly Ala Phe Ser Leu Trp Gly Gly Gly Phe Leu
180      185      190
Phe His Trp Gly Val Ile Asp Tyr Cys Gly Gly Tyr Val Ile His Val
195      200      205
Ser Ala Gly Ile Ala Gly Phe Thr Ala Ala Tyr Trp Val Gly Pro Arg
210      215      220
Ala Gln Lys Asp Arg Glu Arg Phe Pro Pro Asn Asn Ile Leu Phe Thr
225      230      235      240
Leu Thr Gly Ala Gly Leu Leu Trp Met Gly Trp Ala Gly Phe Asn Gly
245      250      255
Gly Gly Pro Tyr Ala Ala Asn Ser Val Ala Ser Met Ala Val Leu Asn
260      265      270
Thr Asn Ile Cys Thr Ala Met Ser Leu Ile Val Trp Thr Cys Leu Asp
275      280      285
Val Ile Phe Phe Lys Lys Pro Ser Val Val Gly Ala Val Gln Gly Met
290      295      300
Ile Thr Gly Leu Val Cys Ile Thr Pro Ala Ala Gly Val Val Gln Gly
305      310      315      320
Trp Ala Ala Leu Val Met Gly Val Leu Ala Gly Ser Ile Pro Trp Tyr
325      330      335
Thr Met Met Ile Leu His Lys Arg Ser Lys Ile Leu Gln Arg Val Asp
340      345      350
Asp Thr Leu Gly Val Phe His Thr His Gly Val Ala Gly Leu Leu Gly
355      360      365
Gly Leu Leu Thr Gly Leu Phe Ala Glu Pro Thr Leu Cys Asn Leu Phe
370      375      380
Leu Pro Val Ala Asp Ser Arg Gly Ala Phe Tyr Gly Gly Ala Gly Gly
385      390      395      400
Ala Gln Phe Gly Lys Gln Ile Ala Gly Gly Leu Phe Val Val Ala Trp
405      410      415
Asn Val Val Val Thr Ser Leu Ile Cys Leu Ala Ile Asn Leu Leu Val
420      425      430
Pro Leu Arg Met Pro Asp Asp Lys Leu Glu Val Gly Asp Asp Ala Val
435      440      445
His Gly Glu Glu Ala Tyr Ala Leu Trp Gly Asp Gly Glu Met Tyr Asp
450      455      460
Val Thr Lys His Gly Ser Asp Ala Ala Val Ala Pro Val Val Val
465      470      475

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<211> 2177
 <212> PRT
 <213> Oryza sativa

<220>
 <221> PEPTIDE
 <222> (0)...(0)
 <223> line 1C-109-51 polypeptide sequence

<400> 64
 Met Ala Asn Leu Gly Gly Gly Ala Glu Ala His Ala Arg Phe Lys Gln
 1 5 10 15
 Tyr Glu Tyr Arg Ala Asn Ser Ser Leu Val Leu Thr Thr Asp Ser Arg
 20 25 30
 Pro Arg Asp Thr His Glu Pro Thr Gly Glu Pro Glu Thr Leu Trp Gly
 35 40 45
 Arg Ile Asp Pro Arg Ser Phe Gly Asp Arg Ala Val Gln Ala Lys Pro
 50 55 60
 Pro Glu Leu Glu Glu Lys Leu Thr Lys Ser Arg Lys Lys Lys Ala Ala
 65 70 75 80
 Ala Ser Asp Pro Asp Leu His Arg Arg Asp Ala Lys Arg Arg Arg
 85 90 95
 Arg Ala Ala Ala Ala Gln Ser Glu Val Ser Val Leu Ser Leu Thr Asp
 100 105 110
 Asp Val Val Tyr Lys Pro Gln Thr Lys Glu Thr Arg Ala Ala Tyr Glu
 115 120 125
 Ala Leu Leu Ser Val Ile Gln Gln Phe Gly Gly Gln Pro Leu Asp
 130 135 140
 Val Leu Gly Gly Ala Ala Asp Glu Val Leu Ala Val Leu Lys Asn Asp
 145 150 155 160
 Lys Ile Lys Ser Pro Asp Lys Lys Lys Glu Ile Glu Lys Leu Leu Asn
 165 170 175
 Pro Ile Ser Asn Gln Met Phe Asp Gln Ile Val Ser Ile Gly Lys Leu
 180 185 190
 Ile Thr Asp Phe His Asp Ala Ser Ala Gly Asp Ser Ala Ala Ala Pro
 195 200 205
 Ser Gly Asp Gly Met Asp Thr Ala Leu Asp Asp Asp Ile Gly Val Ala
 210 215 220
 Val Glu Phe Glu Glu Asn Glu Asp Asp Glu Glu Ser Asp Phe Asp Gln
 225 230 235 240
 Val Gln Asp Asp Leu Asp Glu Asp Glu Asp Asp Asp Leu Pro Glu Ser
 245 250 255
 Asn Ala Pro Gly Ala Met Gln Met Gly Gly Glu Leu Asp Asp Asp Asp
 260 265 270
 Met Gln Asn Ser Asn Glu Gly Leu Thr Ile Asn Val Gln Asp Ile Asp
 275 280 285
 Ala Tyr Trp Leu Gln Arg Lys Val Ser Gln Ala Tyr Glu Asp Ile Asp
 290 295 300
 Pro Gln His Ser Gln Lys Leu Ala Glu Glu Ile Leu Lys Ile Ile Ala
 305 310 315 320
 Glu Gly Asp Asp Arg Asp Val Glu Asn Arg Leu Val Met Leu Leu Asp
 325 330 335
 Tyr Glu Lys Phe Asp Leu Ile Lys Leu Leu Leu Arg Asn Arg Leu Lys
 340 345 350
 Ile Val Trp Cys Thr Arg Leu Ala Arg Ala Glu Asp Gln Glu Gln Arg
 355 360 365
 Lys Lys Ile Glu Glu Asp Met Met Gly Asn Pro Thr Leu Thr Pro Ile
 370 375 380
 Leu Glu Gln Leu His Ala Thr Arg Ala Ser Ala Lys Glu Arg Gln Lys
 385 390 395 400
 Asn Leu Glu Lys Ser Ile Arg Asp Glu Ala Lys Arg Leu Thr Lys Ser
 405 410 415
 Glu Asn Thr Gly Ile Asp Gly Ala Arg Asp Arg Arg Ala Val Asp Arg

425

Page 59

20010-04USA.ST25.txt

Ile Ser Arg Leu Ala Asp Gln Leu Asn Ala Glu Ile Val Leu Gly Thr
 930 935 940
 Ile Gln Asn Ala Arg Glu Ala Cys Ser Trp Leu Gly Tyr Thr Tyr Leu
 945 950 955 960
 Tyr Ile Arg Met Leu Arg Asn Pro Thr Leu Tyr Gly Leu Pro Ala Asp
 965 970 975
 Ile Met Glu Thr Asp Lys Thr Leu Asp Glu Arg Arg Ala Asp Leu Val
 980 985 990
 His Ser Ala Ala Asn Leu Leu Asp Arg Asn Asn Leu Ile Lys Tyr Asp
 995 1000 1005
 Arg Lys Thr Gly Tyr Phe Gln Val Thr Asp Leu Gly Arg Ile Ala Ser
 1010 1015 1020
 Tyr Tyr Tyr Ile Ser His Gly Thr Ile Ser Thr Tyr Asn Glu Tyr Leu
 1025 1030 1035 1040
 Lys Pro Thr Met Gly Asp Ile Glu Leu Cys Arg Leu Phe Ser Leu Ser
 1045 1050 1055
 Glu Glu Phe Lys Tyr Val Ser Val Arg Gln Asp Glu Lys Met Glu Leu
 1060 1065 1070
 Ala Lys Leu Leu Asp Arg Val Pro Ile Pro Val Lys Glu Ser Leu Glu
 1075 1080 1085
 Glu Pro Ser Ala Lys Ile Asn Val Leu Leu Gln Ala Tyr Ile Ser Arg
 1090 1095 1100
 Leu Lys Leu Glu Gly Leu Ser Leu Ser Ser Asp Met Val Tyr Ile Arg
 1105 1110 1115 1120
 Gln Ser Ala Gly Arg Leu Leu Arg Ala Leu Phe Glu Ile Val Leu Lys
 1125 1130 1135
 Arg Gly Trp Ala Gln Leu Ala Glu Lys Ala Leu Asn Leu Cys Lys Met
 1140 1145 1150
 Ile Asp Lys Gln Met Trp Asn Val Gln Thr Pro Leu Arg Gln Phe Pro
 1155 1160 1165
 Gly Ile Pro Lys Glu Ile Leu Met Lys Leu Glu Lys Lys Glu Leu Ala
 1170 1175 1180
 Trp Glu Arg Tyr Tyr Asp Leu Ser Ser Gln Glu Ile Gly Glu Leu Ile
 1185 1190 1195 1200
 Arg Phe Pro Lys Met Gly Arg Gln Leu His Lys Cys Ile His Gln Leu
 1205 1210 1215
 Pro Lys Leu Asn Leu Ser Ala His Val Gln Pro Ile Thr Arg Thr Val
 1220 1225 1230
 Leu Gly Phe Glu Leu Thr Ile Thr Pro Asp Phe Gln Trp Asp Asp Lys
 1235 1240 1245
 Val His Gly Tyr Val Glu Pro Phe Trp Val Ile Val Glu Asp Asn Asp
 1250 1255 1260
 Gly Glu Asn Ile Leu His His Glu Tyr Phe Met Val Lys Lys Gln Tyr
 1265 1270 1275 1280
 Val Asp Glu Asp His Thr Leu Asn Phe Thr Val Pro Ile Tyr Glu Pro
 1285 1290 1295
 Leu Pro Pro Gln Tyr Phe Ile Arg Val Val Ser Asp Lys Trp Leu Gly
 1300 1305 1310
 Ser Gln Thr Ile Leu Pro Val Cys Phe Arg His Leu Ile Leu Pro Glu
 1315 1320 1325
 Lys Tyr Ala Pro Pro Thr Glu Leu Leu Asp Leu Gln Pro Leu Pro Val
 1330 1335 1340
 Thr Ala Leu Arg Asn Ala Arg Tyr Glu Gly Leu Tyr Ser Ala Phe Lys
 1345 1350 1355 1360
 His Phe Asn Pro Ile Gln Thr Gln Val Phe Thr Val Leu Tyr Asn Thr
 1365 1370 1375
 Asp Asp Ser Val Leu Val Ala Ala Pro Thr Gly Ser Gly Lys Thr Ile
 1380 1385 1390
 Cys Ala Glu Phe Ala Ile Leu Arg Asn His Gln Lys Ala Val Ser Gly
 1395 1400 1405
 Glu Ser Asn Met Arg Val Val Tyr Ile Ala Pro Ile Glu Ala Leu Ala
 1410 1415 1420
 Lys Glu Arg Tyr Arg Asp Trp Glu Gln Lys Phe Gly Glu Phe Ala Arg

20010-04USA.ST25.txt

1425 Val Val Glu Leu Thr Gly Glu Thr Ala Ala Asp Leu Lys Leu Leu Asp 1440
 Lys Gly Glu Ile Ile Ile Ser Thr Pro Glu Lys Trp Asp Ala Leu Ser 1455
 Arg Arg Trp Lys Gln Arg Lys Gln Val Gln Gln Val Ser Leu Phe Ile 1470
 Val Asp Glu Leu His Leu Ile Gly Ser Glu Lys Gly His Val Leu Glu 1485
 Val Ile Val Ser Arg Met Arg Arg Ile Ala Ser His Ile Gly Ser Asn 1500
 Ile Arg Ile Val Ala Leu Ser Ala Ser Leu Ala Asn Ala Lys Asp Leu 1515
 Gly Glu Trp Ile Gly Ala Thr Ser His Gly Leu Phe Asn Phe Pro Pro 1530
 Ala Val Arg Pro Val Pro Leu Glu Ile His Ile Gln Gly Val Asp Ile 1545
 Ala Asn Phe Glu Ala Arg Met Gln Ala Met Thr Lys Pro Thr Tyr Thr 1560
 Ala Ile Thr Gln His Ala Lys Asn Gly Lys Pro Ala Leu Val Phe Val 1575
 Pro Thr Arg Lys His Ala Arg Leu Thr Ala Leu Asp Leu Cys Ala Tyr 1590
 Ser Ser Ala Glu Gly Gly Gly Thr Pro Phe Leu Leu Gly Ser Glu Asp 1605
 Glu Met Asp Ala Phe Thr Gly Gly Ile Ser Asp Glu Thr Leu Lys Tyr 1620
 Thr Leu Lys Cys Gly Val Gly Tyr Leu His Glu Gly Leu Ser Asp Leu 1635
 Glu Gln Glu Val Val Thr Gln Leu Phe Leu Ser Gly Arg Ile Gln Val 1645
 Cys Val Ala Ser Ser Thr Val Cys Trp Gly Arg Ser Leu Pro Ala His 1660
 Leu Val Val Val Met Gly Thr Gln Tyr Tyr Asp Gly Arg Glu Asn Ala 1675
 His Thr Asp Tyr Pro Ile Thr Asp Leu Leu Gln Met Met Gly His Ala 1690
 Ser Arg Pro Leu Gln Asp Asn Ser Gly Lys Cys Val Ile Leu Cys His 1705
 Ala Pro Arg Lys Glu Tyr Tyr Lys Lys Phe Leu Phe Glu Ala Phe Pro 1720
 Val Glu Ser His Leu His His Phe Leu His Asp His Met Asn Ala Glu 1735
 Val Val Val Gly Val Ile Glu Asn Lys Gln Asp Ala Val Asp Tyr Leu 1750
 Thr Trp Thr Phe Met Tyr Arg Arg Leu Thr Lys Asn Pro Asn Tyr Tyr 1765
 Asn Leu Gln Gly Val Ser His Arg His Leu Ser Asp His Leu Ser Glu 1780
 Leu Val Glu Thr Val Leu Asn Asp Leu Glu Ser Ser Lys Cys Val Ala 1795
 Ile Glu Glu Asp Met Tyr Leu Lys Pro Leu Asn Leu Gly Leu Ile Ala 1810
 Ser Tyr Tyr Tyr Ile Ser Tyr Thr Thr Ile Glu Arg Phe Ser Ser Met 1825
 Leu Thr Gln Lys Thr Lys Met Lys Gly Leu Leu Glu Ile Leu Ala Ser 1840
 Ala Ser Glu Tyr Ala Glu Leu Pro Ser Arg Pro Gly Glu Glu Asp Phe 1855
 Ile Glu Lys Leu Val Arg His Gln Arg Phe Ser Ile Glu Lys Pro Arg 1870
 Tyr Gly Asp Pro His Val Lys Ala Asn Ala Leu Leu Gln Ala His Phe 1885
 1905 1910 1915 1920 1925 1930 1935

20010-04USA.ST25.txt

Ser Arg His Thr Ile Leu Gly Asn Leu Ala Ala Asp Gln Arg Glu Ile
1940 1945 1950
Leu Leu Ser Ala His Arg Leu Leu Gln Ala Met Val Asp Val Ile Ser
1955 1960 1965
Ser Asn Gly Trp Leu Thr Leu Ala Leu Asn Ala Met Glu Leu Ser Gln
1970 1975 1980
Met Val Thr Gln Gly Met Trp Asp Arg Asp Ser Val Leu Leu Gln Leu
1985 1990 1995 2000
Pro His Phe Thr Lys Glu Leu Ala Arg Arg Cys Gln Glu Asn Glu Gly
2005 2010 2015
Arg Pro Ile Glu Ser Ile Phe Asp Leu Ala Glu Met Ser Ile Asp Glu
2020 2025 2030
Met Arg Asp Leu Leu Gln Gln Ser Asn Pro Gln Leu Gln Asp Ile Ile
2035 2040 2045
Glu Phe Phe Lys Arg Phe Pro Asn Val Asp Met Ala Tyr Glu Val Arg
2050 2055 2060
Glu Gly Asp Asp Ile Arg Ala Gly Asp Asn Val Thr Val Gln Val Thr
2065 2070 2075 2080
Leu Glu Arg Asp Met Thr Asn Leu Pro Ser Glu Val Gly Pro Val His
2085 2090 2095
Ala Pro Arg Tyr Pro Lys Pro Lys Glu Gly Trp Trp Leu Val Ile
2100 2105 2110
Gly Asp Ser Ser Thr Asn Gln Leu Leu Ala Ile Lys Arg Val Ala Leu
2115 2120 2125
Gln Lys Arg Ala Arg Val Lys Leu Glu Phe Thr Ala Ala Ser Glu Ala
2130 2135 2140
Gly Arg Lys Glu Tyr Met Ile Tyr Leu Met Ser Asp Ser Tyr Leu Gly
2145 2150 2155 2160
Cys Asp Gln Glu Tyr Glu Phe Thr Val Asp Val Met Asp Ala Gly Gly
2165 2170 2175
Asp

<210> 65

<211> 181

<212> PRT

<213> Oryza sativa

<220>

<221> PEPTIDE

<222> (0)...(0)

<223> line 1C-056-07 polypeptide sequence

<400> 65

Met Val Gly Cys Leu Ala Thr Ser Thr Lys Thr Ile Leu Ala Glu Ser
1 5 10 15
Leu Leu His Gly Tyr Lys Phe Asp Ser Ile Asn Thr Val Tyr Tyr Met
20 25 30
Ala Pro Phe Ala Thr Met Ile Leu Ala Leu Pro Ala Val Leu Leu Glu
35 40 45
Gly Gly Gly Val Val Thr Trp Phe Tyr Thr His Asp Ser Ile Ala Ser
50 55 60
Ala Leu Val Ile Ile Ile Gly Ser Gly Val Leu Ala Phe Cys Leu Asn
65 70 75 80
Phe Ser Ile Phe Tyr Val Ile His Ser Thr Thr Ala Val Thr Phe Asn
85 90 95
Val Ala Gly Asn Leu Lys Val Ala Val Ala Val Leu Val Ser Trp Leu
100 105 110
Ile Phe Arg Asn Pro Ile Ser Pro Met Asn Ala Ile Gly Cys Ala Ile
115 120 125
Thr Leu Val Gly Cys Thr Phe Tyr Gly Tyr Val Arg His Leu Ile Ser
130 135 140

20010-04USA.ST25.txt

Gln Gln Gln Ala Val Ala Pro Gly Thr Gly Ser Pro Thr Thr Ser Gln
 145 150 155 160
 Thr Asn Ser Pro Arg Ser Arg Met Glu Met Leu Pro Leu Val Gly Asp
 165 170 175
 Lys Gln Glu Lys Val
 180

<210> 66
 <211> 793
 <212> PRT
 <213> Oryza sativa

<220>
 <221> PEPTIDE
 <222> (O)...(O)
 <223> line 1C-100-32 polypeptide sequence

<400> 66
 Met Glu Met Glu Met Glu Asp Asn Lys Ala Pro Ser Pro Pro Ser Pro
 1 5 10 15
 Met Glu Ser Asp Val Ala Glu Glu Lys Arg Lys Arg Glu Asp Asp Ala
 20 25 30
 Ser Ser Ser Ala Val Leu Ala Ala Ala Asn Asn Thr Gly Gly Ala Gln
 35 40 45
 His Pro Met Trp Lys Thr Ser Leu Cys Ser Phe Phe Arg Arg Arg Ala
 50 55 60
 Ala Ser Ser Ala Asp Gly Cys Ser His Gly Asp Ser Cys Arg Tyr Ala
 65 70 75 80
 His Ser Glu Glu Glu Leu Arg Pro Arg Pro Asp Gly Thr Trp Asp Pro
 85 90 95
 Thr Ser Asp Arg Ala Lys Lys Leu Arg Lys Val Ala Ala Asp Glu Val
 100 105 110
 Glu Glu Glu Val Val Thr Ile Asp Lys Ala Leu Asp Lys Cys Leu
 115 120 125
 Val Gly Leu Pro Arg Gly Trp Ala Asn Asp Arg Leu Lys Thr Phe Leu
 130 135 140
 Gln Asp Lys Ala Arg Thr Asn Tyr Ser Ser Ile Leu Pro Pro Ala Leu
 145 150 155 160
 Leu Leu Gly Ile Ser Tyr Ala Thr Ala Lys Lys Lys Gly Met Thr
 165 170 175
 Val Gly Phe Val Thr Phe Glu Asn Ile Glu Gln Leu Lys Asn Ala Ile
 180 185 190
 Glu Val Leu Thr Glu Asn Gln Ser Gly Gly Lys Glu Ile Lys Ile Ala
 195 200 205
 Asp Ala Asn Arg Arg Ser His Gln Lys Leu His Thr Glu Lys Pro Val
 210 215 220
 Ser Asp Asn Gly Val Thr Thr Glu Asn Gly Thr Ser Val Asp Val Pro
 225 230 235 240
 Pro Gly Glu Thr Ser Ala Pro Glu Ala Ala Ile Ser Asn Lys Lys Ser
 245 250 255
 Val Arg Asp Ala Val Thr Pro Leu Ala His Met Ser Tyr Asn Asp Gln
 260 265 270
 Leu Glu His Lys Asn Asn Ser Val Ala Gln Ile Leu Lys Arg Leu Thr
 275 280 285
 Arg Asn Ala Arg Lys Ala Cys Pro Thr Gly Ile Pro Leu Pro Asp Trp
 290 295 300
 Val Phe Lys Ser Lys Glu Ile Gly Gly Leu Pro Cys Lys Leu Glu Gly
 305 310 315 320
 Ile Leu Glu Ser Pro Val Ile Asn Gly Tyr Arg Asn Lys Cys Glu Phe
 325 330 335
 ser Val Gly Phe Ser Leu Glu Gly Lys Lys Thr Val Gly Phe Met Leu
 340 345 350

20010-04USA.ST25.txt

Gly Asn Phe Ser Thr Asp Met Ile Asp Lys Thr Lys Ser Arg Glu Gly
 Val Thr 355 Ala Val Glu Glu Pro 360 Val Asp Cys Pro Asn 365 Val Ser Glu Ile
 Ser Cys Lys Tyr Ala Leu Met Phe Gln Asp Phe Leu Gln Ser Ser Ser
 385 370 385 390 395 400
 Leu Pro Val Trp Asn Arg Val Asn Asn Cys Gly Phe Trp Arg Gln Phe
 405 415
 Thr Val Arg Glu Gly Arg Cys Arg Ala Gln Ala Val Ala Gln Asn Ala
 420 425 430
 Glu Thr Gln Ile Ser Glu Val Met Leu Ile Val Gln Val Cys Ser Thr
 435 440 445
 Gly Val Asp Asp Ala Val Met Lys Asp Glu Phe Asp Lys Leu Thr Val
 450 455 460
 Ala Leu Gln Gln Gly Ala Ala Thr Cys Ser Pro Leu Pro Leu Thr
 465 470 475 480
 Thr Ile Val Val Gln Asp His Lys Gly Ile Ser Asn Ala Ala Pro Ala
 485 490 495
 Asp Cys Pro Leu Ile Pro Leu Leu Val Pro Lys Val Asp Gln Ser Glu
 500 505 510
 Gly Thr Val Asp Lys Thr Arg Ile His Asp His Ile Gly Asn Leu Trp
 515 520 525
 Phe Ser Ile Ser Pro Thr Ala Phe Phe Gln Val Asn Thr Leu Ala Ala
 530 535 540
 Glu Arg Leu Tyr Thr Leu Ala Gly Asp Trp Ala Asn Leu Asn Ser Gly
 545 550 555 560
 Thr Leu Leu Phe Asp Val Cys Cys Gly Thr Gly Thr Ile Gly Leu Thr
 565 570 575
 Leu Ala His Arg Val Gly Met Val Val Gly Ile Glu Met Asn Glu Ser
 580 585 590
 Ala Val Ser Asp Ala Glu Arg Asn Ala Leu Ile Asn Gly Val Ser Asn
 595 600 605
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 35 40 45
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 Pro Thr Asp Asp Cys Arg Tyr Ala Val Phe Asp Phe Asp Phe Val Thr
 65 70 75 80
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 Thr Ala Ser Arg Ile Arg Ala Lys Ile Leu Tyr Ala Thr Ser Lys Gln
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 Phe Gln Val Glu Gly Ala Ala Glu Asp Gly Arg Lys Pro Ser Ile
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 Trp Asp Thr Phe Ile His Gln Gly Tyr Met Pro Asp Gly Ser Asn Ala
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 Met Tyr Asp Met Gly Leu Asp Ala Tyr Arg Phe Ser Ile Ala Trp Pro
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 Tyr Tyr Asn Asn Leu Ile Asp Glu Leu Ile Met His Gly Ile Gln Pro
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 His Val Thr Ile Tyr His Phe Asp Leu Pro Gln Ala Leu Gln Asp Glu
 145 150 155 160
 Tyr Gly Gly Ile Leu Ser Pro Arg Phe Ile Glu Asp Tyr Ser Ala Tyr
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20010-04USA.ST25.txt

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20010-04USA.ST25.txt

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